5 15:13:08 2004 Thu Aug GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model M protein

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August 5, 2004, 13:28:09; Search time 54 Seconds (without alignments) 2103.409 Million cell updates/sec

1 MDKLDANVSSEEGFGSVEXV......ESQCHPPATSPLVAAQPSDT 402 US-10-018-257A-2 2133 erfect score:

equence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table;

1586107 otal number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

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geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aab59572 Human 5-H Aab59573 Dog 5-HT4 Ada83842 Human HTR Ada83841 Human HTR Aao19909 Human TA4 Non-endog Non-endog Human TA4 Rat 5-HT4 Non-endog Rat 5-HT4 Amino aci Human 5-H Ber Non-endog Serotonin Human ser Non-endog Serotonin Serotonin **Drosophi**l Drosophi] Drosophi] Нишал Description Aac19909 F Abb99742 A Abb96742 A Abb66323 F Aar57032 S Aar57030 F Aar57030 F Aar57030 F Aar57030 F Abb56322 A Abb56322 A Abb56322 A Abb56322 A Aau38945 | Adc35817 | Aar15498 | Aar38364 | Aar57033 Aar57031 AA019905 AAR57030 ABB56325 ABB56324 ABB56326 AAR57029 ADC35817 AAR15498 AAR38364 AAB59572 AA019909 ABB99742 ABB56323 AAR57032 AAR57033 AAU38945 AAY14521 8 Query Match Length 380 380 380 387 2069 2042 2042 2042 2042 2042 2042 2003 11879 11879 11874 11874 1873 1869.5 1755 919 598.5 598.5 598.5 582.5 582.5

Abb56347 Non-endog	Abp81807 Human dop	Adc86175 Human GPC	Abg75676 Human D1A	Add26057 Human dop	Aar15499 Rat dopam	Abm04785 Rat dopam	Aar30501 N-termina	Aar21082 Dopamine	Aar30497 N-termina	Abb56350 Non-endog	Abp81808 Human dop	Aar31046 Rat D1B d	Aaw09795 Dl dopami	Aar79381 Dopamine	Aaw40802 Human D5	Aarl3729 Human bet	Abq75674 Human bet	Aaw44932 Canine be	Aar13596 D1 dopami
ABB56347	ABP61807	ADC86175	ABG75676	ADD26057	AAR15499	ABM04785	AAR30501	AAR21082	AAR30497	ABB56350	ABP81808	AAR31046	AAW09795	AAR79381	AAW40802	AAR13729	ABG75674	AAW44932	AAR13596
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human 5-HT4(h) receptor splice variant. AAB59572 standard; protein; 426 AA (first entry) 23-MAR-2001 AAB59572; AAB5957

Human; 5-HT4(h) receptor; 5-hydroxytryptamine; HT; serotonin; oesophageal disorder; asthma; bronchitis; pneumonia; irritable bowel syndrome; cancer; cytostatic; antiasthmatic; antiinflammatory; vulnerary; antisense gene therapy.

WO200077199-A1. Homo sapiens.

21-DEC-2000.

14-JUN-2000; 2000WO-EP005592.

99GB-00013850 14-JUN-1999;

(JANC) JANSSEN PHARM NV.

Van Oers IP, Jurzak M, Luyten WHML; Bender E, Pindon AN,

WPI; 2001-071270/08. N-PSDB; AAF23986.

Novel human 5-HT4 receptor splice variant useful for treating heartburn, reflux, esophagitis, Barrett's esophagus, esophageal cancer, achalasia, reflux, esophagitis, Barrett's esophagus, esophageal stenosis and esophageal spasms

Claim 19; Fig 1B; 64pp; English.

The present sequence is the human 5-hydroxytryptamine (HT)4(h) (serotonin) receptor protein. The protein is useful as a medicament for treating heartburn, refilux, oesophagitis, Barrett's oesophagea, oesophageal cancer, achalasia, oesophageal motility disorders, oesophageal hiatal harnia or other oesophageal motility disorders, oesophageal irritation, such as asthma, bronchospaems, aspiration and its consequences (bronchitis, (broncho) pneumonia, bronchicatasia) and other diseases of the lower oesophageal sphincter, irritable bowel syndrome, denervation of the oesophages (e.g. after certain types of trauma or surgery), and disturbances in oesophageal innervation. It is useful for

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Gaps

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YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRFILGGTVPC 360
                                  The present sequence is the canine 5-hydroxytryptamine (HT)4(h) as a medicament for treating heartburn, receptor protein. The human HT4(h) receptor protein as useful as a medicament for treating heartburn, reflux, oesophagitis, Barrett's oesophagus, oesophageal cancer, achalasia, oesophageal stenosis, oesophageal initiation, such as asthma, motility disorders, oesophageal irritation, such as asthma, bronchospasms, aspiration and its consequences (bronchitis, (broncho) pneumonia, bronchiectasia) and other diseases of the lower oesophageal after citain types of trauma or surgery), and disturbances in oesophageal innervation. It is useful for treating cancers
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Best Local Similarity 96.8%; Pred. No. 3.3e-217;
Matches 389; Conservative 2; Mismatches 11;
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Disclosure; Fig 1B; 64pp; English.
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22-OCT-2001; 2001US-0330457P.
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                                                                                      Length 426;
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                                                                                      Score 2133; DB 4;
Pred. No. 3.6e-224;
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0; Mismatches
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      treating cancers
                                             Sequence 426 AA;
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ADA83841

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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all BSTs expressed in normal tissue in order to identify ESTS that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably as a tumour cell, and the predetermined phenotype is a stress induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell, and for regulating or the preventing the absence or presence of peptides encoded by tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a tumour-associated antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                                                                                                Lobashev AV, Krukovskaya LL;
                                                                                                                                                                                                                Kozlov AP,
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19-FEB-2002; 2002US-0357144P.
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                                                                                                        (BIOM-) BIOMEDICAL CENT
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Sequence 388 AA;

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226
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                                                                                                                                      1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
                                                                                                         1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
                                                                                                                                                                                                                                                                                                                                                                                                               181 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IEKRKFNONSNSTYCVFWVNKPYAITCSVVAPYIPPLLMVLAYYRIYVTAKEHAHOI
                                                                                                                                                                                                                                                                                                                                          AICCOPLYYRNKMTPLRIALMLGGCWVIPTFISFLPIMOGWNNIGIIDL------
                                                          Gaps
                                                    0; Indels 14;
95.7%; Score 2042; DB 6; Length 388; 96.5%; Pred. No. 2.9e-214; ive 0; Mismatches 0; Indels 1
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Query Match
Best Local Similarity 96.5
Matches 388; Conservative
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1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKINYFIV 60

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DA83841

1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV

95.7%; Score 2042; DB 6; Length 388; 96.5%; Pred. No. 2.9e-214; ive 0; Mismatches 0; Indels 14

Best Local Similarity 96.5 Matches 388, Conservative

Similarity

Query Match

Sequence 388 AA;

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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTs) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably axabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress induced phenotype such as hyperosmotic stress or high salt conditions. A method of the inventing the growth of a tumour cell, and for regulating or cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful as an immunated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a tumour-associated markers. A polypeptide of the invention is useful as an immunated antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                               human; marker; expressed sequence tag; EST; arabidopsis; tumour;
stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
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standard; protein; 388 AA
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22-OCT-2001; 2001US-0330457P.
19-PEB-2002; 2002US-0357144P.
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                                                                                                                                                                                                                                                                              Human HTR45 protein.
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                                                                                           ADA83841;
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121 AICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
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Human; trace amine receptor; TAS receptor; G protein-coupled receptor; GPCR; chromosome 6; haematological disorder; CNS disorder; asthma; chronic obstructive pulmonary disease; COPD; cardiovascular disorder; gastrointestinal disorder; cancer; diabetes; obesity;
                                                                                                                                                                                                                                                                                                OMLORAGASSESRPOSADOHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID
                                                                                                                                                                                                                                                                                                                     YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSPRRAFLIILCCDDERYRRPSILGQTVPC
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                                                                          SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                                                                                         191 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                    ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a protein 31% identical to human TAS receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                               402
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17-APR-2002; 2002US-0372809P.
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ABB99742
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                                                                                                                               QMLQRAGASSESRPQSADQHSTHRMRTETXAAKTLCIIMGCPCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                        YTVPQQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDRRYRRPSILGQTVPC 360
                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of human TAA receptor. Which is a G-protein coupled receptor. The sequences are useful in the treatment of hematological disorders, chronic obstructive pulmonary disease, asthma, cardiovascular disorders, central nervous system (CNS) disorders, diabetes, obesity, cancer and genito-urinary disorders. The present sequence is a probe protein used to determine the expression levels of the human T4 receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, G-protein coupled receptor; TA4 receptor; receptor; cytostatic; haemostatic; antiasthmatic; cardiant; antidiabbetic; anorectic; asthma; neuroprotective, haematological disorder; COPD; cardiovascular disease; CNS disorder; diabetes; obesity; cancer; genito-urinary disorder; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotide encoding G-protein coupled receptor, TA4 receptor, useful for treating hematological disorders, asthma, cardiovascular disorders, diabetes, obesity, cancer and genito-urinary disorders.
                                                                                ---IEKRKFNQNSNSTYCVFWVNKPYAITCSVVAFYIPFLLMVLAYYRIYVIAYTAKEHAHQI
                                                           FHAIBKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHOI
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   AICCOPLYYRNGATPLRIALMIGGCWYIPTFISFLFINGGWNNIGIIDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TA4 receptor expression assay probe protein.
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Pred. No. 2.9e-214;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein; 388
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2001US-0331393P.
2002US-0372811P.
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Matches 388; Conservative
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15-NOV-2001; 2
17-APR-2002; 2
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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; growth-related disease; cell regeneration-related disease; Also, cancer; immunological-related cell proliferative disease; autoimmune disease. Alzheimer's disease; alpoilferative disease; autoimmune disease; also secoporosis; cardiomyopathy; inflammation; cooln's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis, anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
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modulating the activity of the GPCR in a disease, e.g. haematological disorders, a CNS disorder, chronic obstructive pulmonary disease (COPD) asthma, a cardiovascular disorder, a gastrointestinal disorder, cancer, diabetes, obesity or genitourinary disorder.
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                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                              Length 388;
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                                                                                                                                                                                      Score 2042; DB 6;
Pred. No. 2.9e-214;
0; Mismatches 0;
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                                                                                                                                                                                                                                              Matches 388; Conservative
                                                                                                                                                                                                                  Similarity
                                                                                                                                        Sequence 388 AA;
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Burmer GC, Roush CL, Brown JP;

WH: 2003-046718/04.

New isolated antigenic peptides e.g., for G protein-coupled receptors
R-PSDB, AB242612.

New isolated antigenic peptides e.g., for G protein-coupled receptors
FCGRN, useful for diagnosing and designing drugs for treating conditions
in which GPGRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
autoimmune diseases.

XX
Disclosure; Fig 1; 523pp; English.

XX
Disclosure; Fig 1; 523pp; English.

XX
The present invention describes antigenic peptides (1) comprising: (a)
ard one of 1601 sequences (see ABPB2D19 to ABP82B19) of 12-34 anino
acids. Also described: (1) an assay for the detection of a particular GPCR. (1) can be used as GPCR modulators and in
acids a loaded antibody having high specificity and high affinity or
avidity for a particular GPCR. (1) can be used as GPCR modulators and
antibodies. The peptides and antibodies are also useful if or detecting an
antibodies. The peptides and antibodies are also useful if or detecting the
presence or absence of corresponding GPCRs. The antigenic peptides for
CPCRs and antibodies are useful if or diseases, cell
reading immune-related diseases, jerundological-related diseases, or autoinmune diseases, growth-related diseases, cell
regeneration-related diseases, immunological-related diseases, call
regeneration-related diseases, immunological-related diseases, call
regeneration-related diseases, immunological-related diseases, call
regeneration-related diseases, multiple sclerosis, pain, psoriasis,
creating immune diseases, multiple sclerosis, pain, psoriasis,
creating indisease, multiple sclerosis, pain, psoriasis,
creating indisease, multiple sclerosis, hypertension,
loss, epilepsy, asthma, tuberulosis, obesity, nausea, hypertension,
loss, epilepsy, asthma, tuberulosis, obesity, nausea, hypertension,
creating inflammation of the present invention

Morry Match

Sequence 388 AA;

Sequence 388 AA;

Sequence 389 AA;

Sequence 389 AA;

Pred protein giver Match are used in the
Company Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
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                                                                                                                                           SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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                                                                                      1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                           1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                          FHA1EKRKFNQNSNSTYCVFMVNKPYA1TCSVVAFY1PFLLMVLAYYR1YVTAKEHAHQ1
                     14;
                     Indels
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                       0; Mismatches
Best Local Similarity 96.5
Matches 388; Conservative
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66/11/9
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Thu Aug
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241 QMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFPVTNIVDPFID 300 Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions SLAFADLLVSVLVMPFGAIBLVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 AICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNGGLGQD 180 181 FHAIBKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFILMVLAYYRIYVTAKEHAHQI 240 ---IEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPPLLAVLAYYRIYVTAKEHAHQI 226 The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR 1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60 1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV Gaps Human; G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease. 1; Indels 14; 95.5%; Score 2037; DB 4; Length 388; 96.3%; Pred. No. 1e-213; ive 0; Mismatches 1; Indels 14 AICCOPLVYRNXMTPLRIALMLGGCWVIPTFISFLPIMOGWNNIGIIDL-Non-endogenous human GPCR protein, SEQ ID NO: 439 Claim 1; Page 240-242; 394pp; English. Lin I; ABB56323 standard; protein; 388 AA Liaw CW, 07-APR-2000; 2000US-0195747P. 05-APR-2001; 2001WO-US011098 Conservative (AREN-) ARENA PHARM INC Lehmann-Bruinsma K, (first WPI; 2001-648759/74. Best_Local Similarity Matches 387; Conserv N-PSDB; ABI97959 Sequence 388 AA; WO200177172-A2 sapiens. 18-FEB-2002 18-OCT-2001 Synthetic of GPCRs. 61 121 121 170 ABB56323; 61 Query Match Ношо RESULT 8 ABB56323 원 a g ò 셤 ò 셤 8 ઠ

61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 1 MDKLDANVSSEEGFGSVEKVVLLTPLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 5-HT4 gerotonin receptor; 5-HT4R; 5-HT4A; adenylate cyclase; agonist; Mammalian 5-HT4 serotonin receptor, corresp. DNA, probes, anti-sense oligo;nucleotide(s) and antibodies - useful for treating conditions involving abnormal 5-HT4 receptor expression, for screening for antibagonists, prodn. of transgenic animals etc. 14; Gaps Serotonin receptor encoded by full-length human serotonin S10 clone. Query Match 94.4%; Score 2014; DB 2; Length 388; Best Local Similarity 95.0%; Pred. No. 3.3e-211; Matches 382; Conservative 3; Mismatches 3; Indels 1: 402 388 STTTINGSTHVLRDAVECGGWESQCHPPATSPLVAAQPSDT STITINGSTHVLRDAVECGGOWESQCHPPATSPLVAAQPSDT Weinshank RL; Example; Page 96-98; 161pp; English. Branchek TA, Ź AAR57032 standard; protein; 388 93WO-US012586 92US-00996772 (SYNA-) SYNAPTIC PHARM CORP. (revised)
(first entry) Hartig P, WPI; 1994-234695/28. correct PN field.) N-PSDB; AAQ68831. Sequence 388 AA; 24-DEC-1992; W09414957-A2. 22-DEC-1993; Homo sapiens 25-MAR-2003 04-MAR-1995 07-JUL-1994 Gerald C, S10 clone. 361 287 347 AAR57032; AAR57032 RESULT 셤 셤 * K S K S K S K B K B K B K K S X K 심 8 원 ò ઠે ò

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S10 is a 270 bp fragment identified when rat brain cDNA was used as template in a PCR with the degenerate primers 3.17 (AAQ68832) and 5.5 (AAQ68831). The clone represents a potentially new serotonin receptor. By direct PCR analysis of bacterial pools, sib selection and filer hybridisation, two full-length cDNA clones - $10-87, 5.5kb; and $10-95, 4.5kb - were determined. The full length human $10 clones are given in AAQ6881 and AAX57032. Page II describes these sequences as clone $10-95 and page 96 describes them as clone $10-87. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AICCOPLVYRNEMTPLRIALMLGGGWVIPTFISELPIMOGWNNIGIIDLERSLNOGLGQD 180
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226
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FHAIEKRKFNQNSNSTYCVFWVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                               OMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID
                                                                                                                         OMLQRAGASSESRPOSADQHSTHRMRTETKAANTLCIIMGCFCLCWAPFFVTNIVDPFID
                                                                                                                                                                 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC
                        ---IERRKENQNSNSTYCVFWVNKPYAITCSVVAFYIPFLLIVLAYYRIYVTAKEHAHQI
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AAO19905 standard; protein; 388 A019905

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AA019905;

(first entry) 11-AUG-2003

Human TA4 receptor associated protein swissnew/070528/5H4_CAVPO.

Human; G-protein coupled receptor; TA4 receptor; receptor; cytostatic; haemostatic; antiasthmatic; cardiant; antidiabetic; anorectic; asthma; neuroprotective. haematological disorder; COPD; cardiovascular disease; CNS disorder; diabetes; obesity; cancer; genito-urinary disorder.

Homo sapiens

WO2002101043-A2

19-DEC-2002

06-JUN-2002; 2002WO-EP006204

08-JUN-2001; 2001US-0296447P. 15-NOV-2001; 2001US-0331393P. 17-APR-2002; 2002US-0372811P.

(FARB) BAYER AG

Zhu 2;

WPI; 2003-148806/14.

Novel polynucleotide encoding G-protein coupled receptor, TA4 recept useful for treating hematological disorders, asthma, cardiovascular disorders, diabetes, obesity, cancer and genito-urinary disorders.

Disclosure; Fig 5; 144pp; English.

The present invention provides the protein and coding sequences of human TA4 receptor, which is a G-protein coupled receptor. The sequences are useful in the treatment of hematological disorders, chronic obstructive pulmonary disease, asthma, cardiovascular disorders, central nervous system (CNS) disorders, diabetes, obesity, cancer and genito-urinary disorders. The present sequence is the protein swissnew/070528/5H4_CAVPO

Sequence 388 AA;

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Length 388;
                              Indele
    Score 1954; DB 6;
Pred. No. 1.2e-204;
B; Mismatches 10;
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  91.6%;
ilarity 92.0%;
Conservative 8
Query Match
Best Local Similarity
Matches 370; Conserv
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1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV

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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated DNA molecule encoding a mammalian 5-HT4 receptor is claimed, having the sequence H2N-Y-X-COOH wherein Y is bp 101-1177 of AAG68828 and X is bps 1127-1267 of AAG68829. S10 is a 270 bp fragment identified when rat brain cDNA was used as template in a PCR with the degenerate primers 3.17 (AAG68832) and 5.5 (AAG68833) derived from well conserved regions among several serotonin receptors in the 3rd and 5th putative transmembrane domains. The peptide sequence corresp. to the 810 PCR clone contd. a transmembrane IV-like domain and the clone represents a potentially new serotonin receptor. By direct PCR analysis of bacterial pools, sib selection and filter hybridisation, two
                SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                           AICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMOGWNNIGIIDLERSLNOGLGOD
                                                                                                                                                ---IEKRKFNQNSNSTYCVFMVNKFYAITCSVVAFYIPFILMVLAYKIYVTAKEHARQI
                                                                                                                                                                                      OMLORAGASSESRPOSADOHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID
                                                                                                                                                                                                                    OVLORAGAPAEGRPOPADOHSTHRMRTETKAAKTLCI IMGCFCLCWAPFFVTNI VDPFID
                                                                                                                                                                                                                                                   YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC
                                                                                                                         FHAIBKRKFNONSNSTYCVFM/NKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-HT4 serotonin receptor; 5-HT4R; 5-HT4A; adenylate cyclase; agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian 5-HT4 serotonin receptor, corresp. DNA, probes, anti-sense oligornucleotide(s) and antibodies - useful for treating conditions involving abnormal 5-HT4 receptor expression, for screening for (ant) agonists, prodn. of transgenic animals etc.
                                                                                 121 AICCOPLVYRNKMTPLRIALMLGGCWVIPMFISFLPIMQGWNNIGIVDL
                                                                                                                                                                                                                                                                                                                                     STTTINGSTHVLRDTVECGGQWESQCHPAASSPLVAAQPIDT 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat 5-HT4 receptor encoded by S10-95 cDNA clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 88-91; 161pp; English
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04-MAR-1995
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hes 359;
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                                                                                                                                                                                 AICCOPLUYRNKWTPLRIALMLGGCWVIPTFISFLPIMOGWNNIGIIDLERSLNOGLGOD 180
                                                                                                                                                                                                                                     ---IEKRKFNHNSNSTFCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAQQI 226
                                                                                                                                                                                                                                                       OMLORAGASSESRPOSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                          YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
full-length cDNA clones (S10-87, 5.5kb; and S10-95, 4.5kb) were determined. The peptide sequences are only 96.7% identical diverging in the second half of the C-terminal tails, downstream of posn. 359. The entire 3' untranslated regions are totally divergent. (Updated on 25-WAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                 1 MDRLDANVSSNEGFGSVEKVVLLTFFAMVILMAILGNLLVMVAVCRDRQLRKIKTNYFIV
                                                                                                                                                                                          1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                    FHALEKRKFNONSNSTYCVFMVNKPYALTCSVVAFYLPFLLMVLAYYRLYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; serotonin receptor; splice variant; alternative splicing; 5-HT
screening; ligand; central nervous system; CNS; disorder; expression;
gastrointestinal disorder.
                                                                                           Gape
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                                                                                                                                                                                                                                                                                                                                       STITINGSTHVLRDAVECGGOWESOCHPPAISPLVAAQP 399
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human serotonin receptor splice variant 5-HT-4(d)
                                                                                           17;
                                                                         88.1%; Score 1879; DB 2;
89.0%; Pred. No. 2.1e-196;
ive 13; Mismatches 17;
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                                                                                           Matches 355; Conservative
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                                                                                   Similarity
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                                                         Sequence 406 AA;
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                                                                                            This sequence represents the amino acid sequence for the human serotonin receptor splice variant 5-HT4(d). 5-HT4(d) and 5-HT4(c) (AAY14521) receptor polypeptides can be used to screen for substances, especially ligands, useful in the treatment of CN3 disorders associated with abnormal 5-HT4(c) receptor expression or gastrointestinal disorders associated with abnormal 5-HT4(d) receptor expression
                                                                                                                                                                                                                                                                                                                                                               9
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  vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eceptor; splice variant; alternative splicing; 5-HT4; central nervous system; CNS; disorder; expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTVPQQWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGGTVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                            SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMLORAGASSESRPOSADOHSTHRMRTETKAAKTICIIMGCFCLCWAPFFVTNIVDPFID
                                                                                                                                                                                                                                                                                                                                                          1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---IEKRKFRONSNSTYCVFWVNKFYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                           Gaps
- and corresponding DNA,
                                                                                                                                                                                                                                                                                                                       14:
                                                                                                                                                                                                                                                                                 Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human serotonin receptor splice variant 5-HT-4(c)
                                                                                                                                                                                                                                                                               88.0%; Score 1878; DB 2; 96.2%; Pred. No. 2.3e-196; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
Splice variants of human 5-HT4 receptor antibodies, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                            Claim 1; Page 44-45; 58pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97FR-00015037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal disorder.
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STTTINGSTHVLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening, ligand,
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                               Sequence 360 AA;
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Human; G protein-coupled receptor; GPCR; non-enconstitutively activated GPCR; agonist; disease
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                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 240; 394pp; English
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          05-APR-2001; 2001WO-US01109B
                                                        07-APR-2000; 2000US-0195747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.5%;
Matches 359; Conservative
                                                                                                                                                            Lehmann-Bruinsma K,
                                                                                                           (AREN-) ARENA PHARM
                                                                                                                                                                                                               2001-648759/74
                                                                                                                                                                                                                                          N-PSDB; AB197958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 387 AA;
                                                                                                                                                                                                                                                                                       Identifying
                                                                                                                                                                                                                                                                                                                                                GPCRs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAPLIILCCDDERYRPSILGQTVPC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the amino acid sequence for the human serotonin receptor splice variant 5-HT4(c). 5-HT4(c) and 5-HT4(d) (AAX14522) receptor polypeptides can be used to screen for substances, especially ligands, useful in the treatment of CNS disorders associated with abnormal 5-HT4(c) receptor expression or gastrointestinal disorders associated with associated with abnormal 5-HT4(d) receptor expression
                                                                                                                                                              vectors,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IEKRKFNDNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
        ö
     Blondel
                                                                                                                                                            corresponding DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 380;
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     ΣÌ
     Gastineau
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1877; DB 2;
Pred. No. 3.2e-196;
0; Mismatches 4;
                                                                                                                                                    variants of human 5-HT4 receptor - and
  Dahmoune Y,
                                                                                                                                                                                                                            Claim 1; Page 41-42; 58pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB56322 standard; protein; 387
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  Langlois M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.2%;
Matches 359; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                           WPI; 1999-349539/30
N-PSDB; AAX79306.
Fischmeister R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 380 AA;
                                                                                                                                                                              antibodies, etc
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Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLAFADILLVSVLVMPPGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AICCOPLVYRNKWTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLILLCCDDERYRRPSILGGTVPC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMLORAGASSESRPOSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFID 300
                                                                                                                                                                                                                     The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCRs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDKLDANVSSEEGFGSVEKVVLLIFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 YTVPGQVWTARLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1874; DB 4;
Pred. No. 6.9e-196;
0; Mismatches 3;
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120

9 9 169 240 226 286

Homo sapiens.

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                                                                                                                                                                                                                                                                        Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therappeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.8%; Score 1873; DB 4; Length 360;
96.0%; Pred. No. 8e-196;
iive 0; Mismatches 1; Indels 14; Gaps
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                                                                                                      05-APR-2001; 2001WO-US011098
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Best Local Similarity 96.0
Matches 358; Conservative
                                                                                                                                                                   (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                           WPI; 2001-648759/74.
N-PSDB; ABI97961.
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                                           WO200177172-A2.
                                                                         18-OCT-2001
              Synthetic.
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Sequence 17, 1
Sequence 8, Al
Sequence 9, Al
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Sequence 1
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Patent No 5766879

GENERAL INFORMATION:
PALL OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
MUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
STATE: NEW YORK

ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.7%; Score 2042; DB 1; Length 388; 96.5%; Pred. No. 5.7e-156; ive 0; Mismatches 0; Indels 1.
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APPLICATION NUMBER: US/08/446,822
FILING DATE: June 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPW/MATTELECOMMUNICATION:
              US-07-626-618A-22
US-08-333-977-22
US-07-966-510-2
US-07-966-591-4
US-07-970-715-4
US-08-444-734A-2
US-08-383-781B-2
US-08-383-781B-2
US-08-383-781B-2
US-08-383-781B-2
US-08-383-781B-2
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US-08-194-338-8
US-08-467-559B-9
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US-08-467-568-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 388 amino acids
amino acid
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Best Local Similarity 96.5
Matches 388; Conservative
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4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

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6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB_pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-314-8
US-09-328-314-4
US-07-936-772A-4
US-08-446-822-4
US-09-555-313B-24
US-09-555-313B-24
US-09-555-313B-24
US-09-555-313B-2
US-09-555-313B-2
US-09-555-313B-2
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US-09-555-313B-2
US-09-328-314-15
US-08-446-822-15
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YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDBRYRRPSILGQTVPC 360
                  287 YIVPGQVWTAPLWLGYINSGLNPFLYAFLAKSFRRAFLILLCCDDERYRRPSILGQTVPC 346
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                                                                                                                                                                                                                        APPLICAT: SYMPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
SITREET: NEW YORK
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                      361 STTTINGSTHVLRDAVECGGGWESQCHPPATSPLVAAQPSDT
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Best Local Similarity 96.5%; Pred. No. 5.7e-156;
Matches 388; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42667-A-PCT/JPW/TEP
                                                                                                                                                                                                                                                                                                                                                              STATE: NEW YORK
ZIP: 1012
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12586
FILING DATE:
                                                                                                                                                                                            Sequence 8, Application PC/TUS9312586 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
CLASSIFICATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,679
REFERENCE/DOCKET NUMBER: 42667
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 664-052
TELEX: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 amino acids
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PCT-US93-12586-8
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                                                                                                                                                             OMLORAGASSESRPOSADOHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
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                                                                                                              ---IEKRKENQNSNSTYCVFWVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
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                                                                                         181 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHOI
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.larity 96.5%; Pred. No. 5.7e-156;
Conservative 0; Mismatches 0;
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Sequence B, Application US/09328314
Patent No. 6331401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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Best Local Similarity
Matches 388; Conserv
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US-09-328-314-8
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                                                                                                                                                                                                                                    Sequence 4, Application US/09328314

Batent No. 6331401

GENERAL INFORMATION:

APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.

APPLICANT: Hartig, Paul R.

APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: Wichard L.

TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
TITLE REPERENCE: 42667-42-PCT-US
CURRENT APPLICATION NUMBER: 08/446,822
EARLIER APPLICATION NUMBER: 08/446,822
EARLIER FILING DATE: 1998-04-03
EARLIER FILING DATE: 1995-07-31
EARLIER FILING DATE: 1995-07-31
EARLIER FILING DATE: 1995-07-31
EARLIER FILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SOUTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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287 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLILLCCDDBRYRRPSILGQTVPC 346
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al Similarity 89.5%; Pred. No. 1.8e-143;
357; Conservative 12; Mismatches 16; Indels 14
                                                                          361 STTTINGSTHVLRDAVECGGOWESQCHPPATSPLVAAQPSDT 402
                                                                                                         STITINGSTHVLRDAVECGGOWESQCHPPATSPLVAAQPSDI 388
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ORGANISM: Rattus norvegicus
3-09-328-314-4
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8-09-328-314-4
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Best Local S
Matches 357
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227 QMLQRAGATSESRPQTADQHSTHRMRTBTKAAKTLCVIMGCFCFCWAPPFVTNIVDPFID 286
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APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Paul R.
APPLICANT: Baranchek, Thereas A.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING 5-HT4A SEROTONIN
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPER & DUMHAM
STRET: 30 ROCKEFELLER PLAZA
CIT: NEW YORK
STATE: NEW YORK
ZIP: 10112
COMPUTER READABLE FORM:
MEDLIM TYPE: PLOYPY disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURSAGE STRIENT PULLOS/MS-LOS
SOFTWARE PETENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/996,772A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGATI INFORMATION:
NAME: White, P. John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42667/JPW/TEP
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAM: (212) 664-0525
TELESA: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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RESULT 6 US-08-446-822-4

Sequence 4, Application US/07996772A Patent No. 5472866 GENERAL INFORMATION:

ESULT 5 S-07-996-772A-4

us-10-018-257a-2.rai

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COMPUTER READABLE FORM:
                                                                                                                                                     CITY: NEW YORK
STATE: NEW YORK
ZIP: 10112
         SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 ---IEKRKFNHNSNSTFCVFMVNKPYALTCSVVAFYIPFLLMVLAYYRIYVTAKGHAQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
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Sequence 4, Application US/08446822
Patent No. 5766879
GENERAL INPORMATION:
APPLICANT: SYNAMIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STITINGSTHVLRDAVECGGQWESQCHPPATSPLVAAQP 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42667-A-PCT-US/JPW/MAT
                                                                                                                                                                                                                            ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/6446,822
FILING DATE: June 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGDNT INCOMMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
                                                                                                                                                        ADDRESSEE: COOPER & DUNHAM STREET: 30 ROCKEFELLER PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-040
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 406 amino acida
amino acid
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Best Local Similarity 89.24
Matches 356; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-446-822-4
                                                                                                                                                                                           CITY: NEW YORK
STATE: NEW YORK
ZIP: 10112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 YTVPGOVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGGTVPC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Gaps
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APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSS:
ADDRESSED: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.3%; Score 1884; DB 5; 1
Best Local Similarity 89.2%; Pred. No. 2.7e-143;
Matches 356; Conservative 13; Mismatches 16;
                                                                                                                                                                                                                                                                                       COMPUTER FRAMEMALE FORMY

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC-COMPATIBLE

COPERATING SYSTEM: PC-DGS/MS-DGS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12586

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT THFORMATION:

NAME: White, P., John

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

TELECHNONE: (212) 977-9550

TELEFRANE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
TOPOLOGY: li--
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LENGTH: 406 amin.
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PCT-US93-12586-4
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PCT-US93-12586-4 Sequence 4, Application PC/TUS9312586

RESULT 8 US-09-555-313B-4 ; Sequence 4, Application US/0955313B ; Patent No. 6506580

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Query Match
Best Local Similarity 95.2
Matches 359; Conservative
     Conservative
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ORGANISM: Homo sapiens
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     359;
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     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTVPQQVWTAFIWLGYINSGLNPFLYAFINKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                        SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMLORAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FICSHMEISTER, Rudolph et al.
TITLE OF INVENTION: Splicing variants of the human serotoninezgic receptor TITLE OF INVENTION: Splicing variants of the human serotoninezgic receptor TITLE OF INVENTION: 5-HT4 and uses thereof, in particular for screening FILE REFERENCE: P06762US00/BAS
CURRENT APPLICATION NUMBER: US/09/555,313B
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                    1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
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in particular for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                     MDKLDANVSSEGFGSVEKVVLLTFLSTV1LMA1LGNLLVMVAVCWDRQLRK1K1NYF1V
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                   14;
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Pred. No. 9e-143;
                                                                                                                                                                                                                                                                                                    Length 360;
                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                 88.0%; Score 1878; DB 4;
96.2%; Pred. No. 7.1e-143;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-09-55-313B-24
Sequence 24, Application US/0955313B
Betent No. 6506580
GENERAL INFORMATION:
APPLICANT: FICSHWEISTER, Rudolph et al.
TITLE OF INVENTION: Splicing variants of the hum
TITLE OF INVENTION: Splicing variants of the hum
TITLE OF INVENTION: 5-HT4 and uses thereof, in
FILE REFERENCE: P06762US00/BAS
CURRENT APPLICATION NUMBER: US/09/55,313B
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: FR 97/15037
PRIOR FILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 380
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95.2%;
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Best Local Similarity 96.2
Matches 359; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                              LENGTH: 360
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in particular for screening
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                                                          1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDROLRKIKTNYFIV
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Fatent No. 6506580
GENERAL INFORMATION:
APPLICANT: FICSHWEISTER, Rudolph et al.
TITLE OF INVENTION: 5-HT4 and uses thereof, in
TITLE OF INVENTION: 5-HT4 and uses thereof, in
FILE REPERENCE: P06762US00/BAS;
CURRENT APPLICATION NUMBER: US/09/555,313B
CURRENT FILING DATE: 2002-08-13
FRIOR FILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
0; Mismatches
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227 QMLQRAGATSESRPQTADQHSTHRMRTETKAAKTLCVIMGCFCFCWAPFFVTNIVDPFID 286
  ---IEKRKFNHNSNSTFCVFMVNKPYAJTCSVVAFYIPFLLMVLAYYRIYVTAKEHAQQI 226
                                                                                                                                          YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
                                                                                                                                                                     287 YIVPEKVWTAPLWLGYINSGLNPFLYAPLNKSFRRAFLIILCCDDERYKRPPILGQTVPC 346
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                                              241 OMLORAGASSESRPOSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATE: SYNAPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
WINNER OF SEQUENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: COOPER & DUNHAM
STREET: 30 ROCKFFELLER PLAZA
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.9%; Score 1769; DB 1; Length 387; 88.7%; Pred. No. 4.1e-134;
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APPLICATION NUMBER: US/08/446,822
FILING ADTE: Unne 1, 1995
CLASSIFICATION: 800
ATTONNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPW/MAT
TELECOMMULICATION INFORMATION:
TELECOMMULICATION 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 391-0525
HFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 338; Conservative
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US-08-446-822-2
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INFORMATION F
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287 YIVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGOTVPC 346
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                                                                                                                                                                                                                         Sequence 2, Application US/07996772A

Sequence 2, Application US/07996772A

Sequence 2, Application US/07996772A

Patent No. 5472866

APPLICANT: Gerald, Christophe

APPLICANT: Hartig, Paul R.

APPLICANT: Branchek, Theresa A.

APPLICANT: Weinshank, Richard L.

TITLE OF INVENTION: DNA ENCODING 5-HT4A SEROTONIN

TITLE OF INVENTION: RECEPTORS AND USES THEREOF

NUMBER OP SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: COOPER & DUNHAM

STREET: NEW YORK

STATE: NEW YORK

SIPH 1012

COMPUTED PT.
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88.7%; Pred. No. 4.1e-134;
iive 11; Mismatches 18;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/996,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
RAGISTRATION NUMBER: 28,678
REFERENCS/DOCKET NUMBER: 42667
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRARACTERISTICS:
                                                                                                                                                                  STTTINGSTHVLRDAVE 377
                                                                                                                                                                                                            347 STTTINGSTHVLSSGTE 363
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amino acid
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Best Local Similarity 88.7
Matches 338; Conservative
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US-07-996-772A-2
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APPLICANT: Gerald, Christophe
APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Faul R.
APPLICANT: Hartig, Faul R.
APPLICANT: Weinshank, Thichard L.
TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
FILE REFERENCE: 42667-42-PCT-08
FURRENT APPLICATION NUMBER: 08/446,822
EARLIER PAPLICATION NUMBER: 08/446,822
EARLIER PILING DATE: 1995-07-31
EARLIER APPLICATION NUMBER: PCT/US93/12586
EARLIER APPLICATION NUMBER: PCT/US93/12586
EARLIER PILING DATE: 1993-12-22
EARLIER PILING DATE: 1993-12-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
LENGTH: 387
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                                                                                                       YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
                                                                                                                                     287 YIVPEKVWIAFLWLGYINSGINPFLYAFLNKSFRRAFLIILCCDDERYKRPPILGQIVPC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDRLDANVSSNRGFGSVEKVVLLTFPAMVILMAILGNLLVMVAVCRDRQLRKIKTNYPIV 60
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                                                                                                                                                                                                                                                             STTTINGSTHVLRYTVLHSGO 367
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09328314 Patent No. 6331401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Rattus norvegicus S-09-328-314-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
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            Sequence 2, Application PC/TUS9312586
GENERAL INFORMATION:
APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DINHAM
STREET: 30 ROCKEFELLER FLAZA
                                                                                                                                                                                                                                                                                                                                                                                                           CLASSITION:
ATTORNEY AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 42667-A-PCT/JPW/TEP
TELECOMNUNICATION INFORMATION:
TELEFAX: (212) 977-9550
TELEFAX: (212) 664-0525
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     MEDIUM TYPE: Flopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/12586 FLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STTTINGSTHVLRDAVECGGQ 381
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amino acid
                                                                                                                                                                                           CITY: NEW YORK
STATE: NEW YORK
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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PCT-US93-12586-2
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127 LVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIEK 186
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RESULT 15
US-08-446-822-15
US-08-446-822-15
i Sequence 15, Application US/08446822
i Patent No. 5766879
i GENERAL INFORMATION:
i TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
I TITLE OF INVENTION: AND USES THEREOF
I TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSES: COOPER & DUNHAM
STREET: 30 RCCKEFELLER PLAZA
CITY: NEW YORK
STREET: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Bloppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Bloppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Date 11 1995
CURRENT APPLICATION NUMBER: US/08/446,822
FILING DATE: JUBBER: 28,678
REFERENCE (212) 278-0400
TELEFRONE (212) 278-0400
TELEFRONE (212) 278-0400
TELEFRONE (212) 231-0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acid
TYPE: amino acid
TYPE: amino acid
WG-08-446-822-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.1%; Score 1239; DB 1; Length 261; Best Local Similarity 93.6%; Pred. No. 7.2e-92; Matches 234; Conservative 0; Mismatches 2; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: August 5, 2004, 13:36:37
Job time : 20 secs
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August 5, 2004, 13:35:20 ; Search time 46.Seconds (without alignments) 2741.316 Million cell updates/sec
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2133
1 MDKLDANVSSEEGFGSVEKV.......ESQCHPPATSPLVAAQPSDT 402
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT MRW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1291235
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1291235 segs, 313682936 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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	Description	Sequence 8, Appli	Sequence 123, App	Sequence 124, App	Seguence 18, Appl	Sequence 439, App	Sequence 3, Appli	Sequence 4, Appli	Seguence 23, Appl	Sequence 436, App	Sequence 443, App	Sequence 441, App	Sequence 445, App	Sequence 2, Appli	Sequence 15, Appl	Sequence 6, Appli	
SUMMALES	ΩI	US-09-989-861-8	US-10-157-031-123	US-10-157-031-124	US-10-225-567A-18	US-09-826-509-439	US-10-092-771-3	US-09-989-861-4	US-10-318-661-23	US-09-826-509-436	US-09-826-509-443	US-09-826-509-441	US-09-826-509-445	US-09-989-861-2	US-09-989-861-15	US-09-989-861-6	
	DB	σ	14	14	14	11	12	σ	14	7	11	11	11	σ	Q	σ	
	% Query Match Length DB	388	388	388	388	388	388	406	387	387	360	380	378	387	261	178	
	% Query Match	95.7	95.7	95.7	95.7	95.5	91.6	88.4	88.1	87.9	87.8	87.8		82.9			
	Score	2042	2042	2042	2042	2037	1954	1886	1879	1874	1873	1872	1869.5	1769	1239	939	
	esult No.	-	71	m	4	'n	9	7	œ	Q,	10	11	12	13	14	15	

Sequence 26, Appl Sequence 69, Appl	Sequence 30, Appl Sequence 487, App	9, 2		628,		4	Ä	'n	Ψ	цı	ਧ	Sequence 20, Appl	Sequence 51, Appl	ব	Sequence 47, Appl	2, 1	Sequence 100, App	8, 1	10	Sequence 4, Appli	Sequence 22, Appl	48	Sequence 24, Appl
US-10-299-642-26 US-10-270-333-69	299-642 826-509		٦,-	-10-292-798-6	US-10-299-642-32	US-10-277-078-4	US-10-299-642-16	US-09-993-844-5	US-10-633-438-62	US-10-092-771-5	US-10-205-331-4	US-10-299-642-20	US-09-964-956-51	US-09-826-509-493	US-09-964-956-47	US-10-277-078-2	US-10-225-567A-100	US-10-299-642-8	US-10-299-642-10	US-10-352-684A-4	US-10-299-642-22	US-09-964-956-48	US-10-299-642-24
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UG-09-989-861-8

Sequence 8, Application US/0989861

Sequence 8, Application US/0989861

Sequence 8, Application US/0989861

Sexuence 8, Application US/09090861

GENERAL INFORMATION:

APPLICANT: Hartig, Paul R.

TITLE OF INVENTION: Theread.

TITLE OF INVENTION: 100 PARCH.

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/328,314

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1992-12-24

NUMBER OF SEQ 1D NOS: 19

SEQ 1D NOS: 19

SEQ 1D NOS: 19

TYPE: PAT

OURTY MATCH

APPLICATION NUMBER: CONSERVENTION NUMBER: 07/996,772

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MATCHES 388; CONSERVATIVE NOT VILLE STULING ADDRIVENT TO THE STULING THE STULING ADDRIVENT TO T
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Db 61 SLAFADLLVSVLVMPFGAIELVQDIMIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 121 AICCQPLVYRNKMTPLAIALAMLGGCWVIPTEISFLPIMOGMNNIGIIDLERSLWQGLGQD 180 121 AICCQPLVYRNKMTPLAIALAMLGGCWVIPTEISFLPIMOGMNNIGIIDL	Qy 361 STTTINGSTHVLRDAVECGGQWESQCHPPATSPLVAAQPSDT 402
RESULT 2 US-10-157-031-123	DB 66 MAILG WASEN
Query Match 95.7%; Score 2042; DB 14; Length 388; Best Local Similarity 96.5%; Pred. No. 6.6e-185; Additional and a conservative 0; Mismatches 0; Indels 14; Gaps 1; Qy 1 MDKLDANVSSEEGFGSVEKVVLITFLSTVILMAILGNLLVMVAVCMDRQLEKIKTNYFIV 60 Conservative Conservative	Db 170IEKRKPNONSNSTYCVFWVNKPYAITCSVVAFYIPFLLMVLAYYRIYTAKEHAAQI 226 Qy 241 QMLQRAGASSESRPQSADQHSTHRWRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300 Db 227 QMLQRAGASSESRPQSADQHSTHRWRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300 Qy 301 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360 Db 287 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 346 QY 361 STTTINGSTHVLRDAVECGGQWESQCHPPATSPLVAAQPSDT 402
181 FHAIEKRKFNONSNSTYCVFWYNKDYAITCSVVAFYIPFLLMVLAYYRIYYTAKEHAHOI 170IERRKFNONSNSTYCVFWYNKDYAITCSVVAFYIPFLLMVLAYYRIYYTAKEHAHOI 170IERRKFNONSNSTYCVFWYNKDYAITCSVVAFYIPFLLMVLAYYRIYYTAKEHAHOI 241 QMLQRAGASSESRPQSADOHSTHRMFTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 227 QMLQRAGASSESRPQSADQHSTHRMFTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 301 YTVPGQVWTAFLMLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGGTVPC	RESULT 4 US-10-225-567A-18 US-10-225-567A-18 Sequence 18, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION: APPLICANT: LifeSpan Biosciences APPLICANT: Burmer, Glenna C. APPLICANT: Rough, Christine L. TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECE! FILE REPERENCE: 1920-4-4 CURRENT APPLICATION NUMBER: US/10/225,567A

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Sequence 3, Application US/10092771

Publication No. US20030064381A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FIGURE SETS COLUMPRES SQUIBD COMPANY
TITLE OF INVENTION: HGPREMYZE, EXPRESSED HIGHLY IN TESTIS AND GASTROINTESTINAL TISS:
TITLE OF INVENTION: HGPREMYZE, EXPRESSED HIGHLY IN TESTIS AND GASTROINTESTINAL TISS:
TITLE OF INVENTION: HGPREMYZE, EXPRESSED HIGHLY IN TESTIS AND GASTROINTESTINAL TISS:
TITLE OF INVENTION: HGPREMYZE, EXPRESSED HIGHLY IN TESTIS AND GASTROINTESTINAL TISS:
TITLE OF INVENTION: WHOMER: US 10/092,771

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US 60/273,963

PRIOR FILING DATE: 2001-03-07

PRIOR FILING DATE: 2001-03-07

NUMBER OF SEQ ID NOS: 76

SEQ ID NOS: 76

SEQ ID NO 3

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Pred. No. 1.4e-176;
B; Mismatches 10;
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Best Local Similarity 92.0%;
Matches 370; Conservative
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US-10-092-771-3
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Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: NO US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR PAPLICATION NUMBER: 06/195,747
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 439
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                                                                                                                                                                                                                                                                           Length 388;
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                                                                                                                                                                                                                                                                      Score 2042; DB 14;
Pred. No. 6.6e-185;
0; Mismatches 0;
  PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 388
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96.5%;
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Matches 387; Conservative
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Best Local Similarity 96.5
Matches 388; Conservative
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ORGANISM: Homo sapiens
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3-10-225-567A-18
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                                                  287 YIVPGQLWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILCGTVPC 346
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                                                                                                                                                                                      Sequence 4, Application US/09989861

Sequence 4, Application US/09989861

Patent No. US20020081661A1

GENERAL INFORMATION:
Hartig, Paul R.
APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
FILE REFERENCE: 42667-Az-PCT-US
CURRENT APPLICATION NUMBER: US/09/989,861
CURRENT FILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
PRIOR FILING DATE: EARLIER FILING DATE: 1992-12-24

NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VET. 2.1
                                 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC
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                                                                                              STTTINGSTHVLRDAVECGGOWESOCHPPATSPLVAAOPSDT 402
                                                                                                                  STITINGSTHVLRDAVECGGOWESOCHPPATSPLVAAQP 399
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US-09-989-861-4
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US-09-989-861-4
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RESULT 8

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% Sequence 436, Application US/09826509

| Sequence 436, Application US/09826509
| Publication No. US20030204073A1
| Publication No. US20030204073A1
| APPLICANT: Lichmann-Bruinsma, Karin APPLICANT: Lichmann-Bruinsma, Karin APPLICANT: Lin, I-Lin
| APPLICANT: Lin, I-Lin
| TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Know TITLE OF INVENTION: Protein-Coupled Receptors
| FILE REFERENCE: AREN-207 | CURRENT APPLICATION NUMBER: US/09/826,509 | CURRENT FILING DATE: 2001-04-05 | PRIOR FILING DATE: 2000-04-07 | PRIOR FILING PRIOR PRIOR FILING PRIOR FILING PRIOR PRIOR FILING PRIOR PRIOR FILING PRIOR PRIOR FILIN
Publication No. US203016747641

Fublication No. US203016747641

GENERAL INFORMATION:

APPLICANT:
CONCALIN.

TITLE OF INVENTION: Selective Target Cell Activation By
TITLE OF INVENTION: Sepression of A G Protein-Coupled Receptor Activated

TITLE OF INVENTION: Superiorly By Synthetic Ligand

FILE REFERENCE: UCAL-049C1P2

CURRENT APPLICATION NUMBER: US/10/318,661

CURRENT FILING DATE: 1999-12-20

FRIOR APPLICATION NUMBER: US 09/341,446

FRIOR FILING DATE: 1999-12-20

FRIOR PRING DATE: 1999-12-20

FRIOR PILING DATE: 1999-03-25

FRIOR PILING DATE: 1999-03-25

FRIOR SEQ ID NOS: 28

SOFTWARE: FASTERQ for Windows Version 4.0

FROM THE SECTION NUMBER: PARTING DATE: 1990-03-26

SEQ ID NO 23

SEQ ID NO 23

FRIOR PARTING DATE: 1991-03-26

SEQ ID NO 23
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Pred. No. 1.9e-169;
0; Mismatches 2;
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Best Local Similarity 95.7%;
Matches 360; Conservative (
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CRGANISM: Homo sapiens
US-10-318-661-23
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APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lia, 1-Lin
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known (TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT RAPPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1998-110-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
LENGTH: 380
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1 MDKLDANVSSEBGFGSVEKVVLLTFLSTVILMAILGNILVWVAVCWDRQLRKIKTNYFIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 441, Application US/09826509; Publication No. US20030204073A1; GENERAL INFORMATION:
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96.0%; Pred. No. 6.3e-169;
iive 0; Mismatches 1;
                                                                                                                                                                       Score 1874; DB 11;
Pred. No. 5.5e-169;
0; Mismatches 3;
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 436
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STTTINGSTHVLRDAV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STITINGSTHVLRYTV 362
                                                                                                                                                                       Query Match
Best Local Similarity 95.5%;
Matches 359; Conservative
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Matches 358; Conservative
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S-09-826-509-443
                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVPCLVRTSLDVLLTTASIFHLCCISLDRYY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 OMLORAGASSESRPOSADOHSTHRWRTETKAAKTICIIMGCFCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 OMLORAGATSESRPOTADOHSTHRMRIETKAAKTLCVIMGCRCPCWAPPFVINIVDPPID 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
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                                                                                                    APPLICANT: Bartig, Fall R.
APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DAR Encoding 5-HT4 Serotonin Receptors And Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 42667-AZ-PCT-US
CURRENT APPLICATION NUMBER: 08/09/989,861
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/328,314
PRIOR PLILING DATE: EARLIER PILING DATE: 1998-04-03
PRIOR PLILING DATE: EARLIER FILING DATE: 1993-12-22
PRIOR PRILOGATION NUMBER: EARLIER APPLICATION NUMBER: CT/US93/12586
PRIOR PLILING DATE: EARLIER FILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SOFTWARR: PATENTING DATE: 1902-12-24
SOFTWARR: PATENTING DATE: 1902-12-24
SOFTWARR: PATENTING DATE: 1003-12-24
SOFTWARR: PATENTING DATE: 1003-12-24
SOFTWARR: PATENTING DATE: 1003-12-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDRLDANVSSNEGFGSVEKVVLLTFFAMVILMAILGNLLVMVAVCRDRQLRKIKTNYFIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 ---IEKRKFNHNSNSTFCVFWVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.9%; Score 1769; DB 9
88.7%; Pred. No. 5e-159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 STTTINGSTHVLRDAVECGGQ 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 STÍTINGSTHVLRYTVLHSGÓ 367
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US-09-989-861-15
Sequence 15, Application US/0999861;
Patent No. US20020081661A1
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe
Sequence 2, Application US/09989861
Patent No. US20020081661A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hartig, Paul R.
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TILLE OF INVENTION: DNA Encoding
TITLE OF INVENTION: Thereof
FILE REFERENCE: 42667-AZ-PCT-US
                                                                                APPLICANT: Gerald, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Rattus norvegicus
US-09-989-861-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.9*
Best Local Similarity 88.7*
Matches 338; Conservative
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US-09-086-509-445

i Sequence 445, Application US/09826509

i Publication No. US20030204073A1

i GENERAL INFORMATION:

APPLICANT: Lian, Chen W.

APPLICANT: Lian, Chen W.

ITILE OF INVENTION: Protein-Coupled Receptors

TITLE OF INVENTION: Protein-Coupled Receptors

TITLE OF INVENTION: Protein-Coupled Receptors

CURRENT APPLICATION NUMBER: US/09/826,509

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589

SOFTWARE: Patentin Version 2.1

SEQ ID NO 445

LENTH: 378
                                  OMLQRAGASSESRPQSADQHSTHRMRTETKAKKTLCIIMGCFCLCWAPPFVTNIVDPFID 286
                                                                                                          YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
                                                                                                                                            YTVPGQVWTAFLWLGYINSGLNFFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 346
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Pred. No. 1.4e-168;
0; Mismatches 3;
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                                                                                                                                                                                                                       STTTINGSTHVLRDAVE 377
                                                                                                                                                                                                                                                                          STITINGSTHVLSSGTE 363
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ilarity 92.8%;
Conservative C
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US-09-826-509-445
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Matches 360;
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CURRENT APPLICATION NUMBER: US/09/989,861 CURRENT FILING DATE: 2001-11-19

RESULT 13 US-09-989-861-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 RKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQRA 246
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/328,314
PRIOR FILING DATE: BARLIER FILING DATE: 1990-04-03
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: PCT/US93/12586
PRIOR PILING DATE: EARLIER FILING DATE: 1993-12-22
PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENT PILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SCFTWARE: PATENT PILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SCFTWARE: PATENT PILING DATE: 1992-12-24
CENTILIER PILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SCFTWARE: PATENT PILING DATE: 1992-12-24
CENTILIER PILING DATE: 1993-12-24
CENTILIER PILING DATE: 1993-12-23
CENTILIER PILING DATE: 1993-12-23
CENTIL
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Pred. No. 5.3e-109;
0; Mismatches 2;
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93.6%;
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Best Local S
Matches 234
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Gaps

127 LVYRNKONTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIEK 186

Query Match
44.0%; Score 939; DB 9; Length 178;
Best Local Similarity 92.2%; Pred. No. 9.1e-81;
Matches 177; Conservative 0; Mismatches 1; Indels 14;

TYPE: PRT ORGANISM: Homo sapiens S-09-989-861-6

Detent No. US20020081661A1
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Paul R.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: UNDER: US/09/989, 861
TITLE OF INVENTION: Thereof
FILE REFERENCE: 42667-AZ-PCT-US
CURRENT APPLICATION NUMBER: US/09/989, 861
CURRENT APPLICATION NUMBER: US/09/989, 861
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/328,314
PRIOR APPLICATION NUMBER: EARLIER PLILNG DATE: 1998-04-03
PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-22
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1993-12-22
RICH APPLICATION NUMBER: EARLIER FILING DATE: 1992-12-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PARENTIN VET. 2.1
SEQ ID NOS: 19

Sequence 6, Application US/09989861 Patent No. US20020081661A1

8-09-989-861-6

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306
                                     107 GASSESRPQSADQHSTHPMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFIDYTVPGQ 166
1 LVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDL-------IEK 46
                                                                                                                    247 GASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFIDYTVPGQ
                                                                                                                                                                                                   307 VWTAFLWLGYIN 318
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OMLORAGASSESRPOSADQHSTHRMRTETXAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
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88888888888888888888888888888888888888		receptor - rat names: 5-HT receptor attus norvegicus (No) a55549; S6649; NG1D 55-HT(4) receptor: mc number: 855549; MUID 855549 1-406 GER> 1-5-HT(4) Receptor: mc number: 85549; MUID 85649; MUID 8649; MUID 8649; MUID 10-16-16-16-16-16-16-16-16-16-16-16-16-16-
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2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3		inin 4 10- 10- 10- 10- 10- 10- 10- 10- 10- 10
U		RESULT 1 95549 Nathernate names: C;Species: Rattus no C;Species: Rattus no C;Species: Rattus no C;Species: Natham R;Gerald, C; Adham R;Gerald, C; Schmu R;Molecule type: mR R;Ullmer, C; Schmu R;Ulmer, C; Schmu R;Ulmer, C; Schmu R;Ulmer, C; Schmu R;Ulmer, C; Schmu R;Molecule type: mR R;Ullmer, C; Schmu R;Cerance number: R;Ulmer, C; Schmu R;Cerance number: R;Ulmer, C; Schmu R;Cerance number: R;Ulmer, C; Schmu R;Cerance number: R;Ceran
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112 CCISLDRYYAICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLER 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 SLNQGLGQDFHAIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYV 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VIEKRKEHQNSNSTYCIFWVNKPYAITCSVVAFYIPFLLMVLAYWAYNTAYWAKHYUTAKEHAHQIQM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCISLDRYYAICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDL-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerotonin receptor 4A - pig (fragment)

NyAlternate names: 5-hydroxytryptamine receptor 4A (5-HTR4A)

C)Species: Sus scrofa domestica (domestic pig)

C)Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000

C)Accession: S66495

R;Ulmer, C.; Schmuck, K.; Kalkman, H.O.; Luebbert, H.

FEBS Lett. 370, 215-221, 1995

A;Title: Expression of serotonin receptor mRNAs in blood vessels.

A;Reference number: S66487; MUID:95385798; PMID:7656980
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NAlterrate names: 5-hydroxytryptamine receptor 4 (5-HTR4)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Oct-1996 #sequence_revision 13-War-1997 #text_change 11-Jan-2000
C;Accession: S66487
R;Pilmer, C.; Schmuck, K.; Kalkman, H.O.; Luebbert, H.
R;Pilmer, C.; Schmuck, K.; Kalkman, H.O.; Luebbert, H.
A;Title: Expression of serotonin receptor mRNAs in blood vessels.
A;Reference number: 866487; MUID:95385798; PMID:7656880
A;Residues:1-144 <ULL>
A;Cross-references: EMBL:248150; NID:9984126; PIDN:CAA88167.1; PID:9984127
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z48176; NID:g984244; PIDN:CAA88199.1; PID:g984245
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCQPLVYRNGATPLRVAVLLAGCWAIPVLISFLPIMQGWNNIGITDLERTSKPRLGQDLH
                                                                                                                                A,Gene: GDB:HTR4
A,Cross-references: GDB:6381308
C,Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; neurotransmitter receptor;
                                                                                                                                                                                                                                                                                                                  Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 TAKEHAHQIQMLQRAGASSESRPQSADQHSTHRMRTET 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 TAKEHAHOIOMLORAGASSESRPOSADOHSTHRMRTET 144
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A,Status: preliminary, nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                              Query Match 35.4%; Score 755; DB 2; L
Best Local Similarity 91.1%; Pred. No. 4.9e-61;
Matches 144; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-151 <ULL>
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NyAlternate names: 5-hydroxytryptamine receptor 4 (5-HTR4)
NyAlternate names: 5-hydroxytryptamine receptor 4 (5-HTR4)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
C;Accession: S66493
R;Ullmer, C.; Schmunck, K.; Kalkman, H.O.; Luebbert, H.
REBS Lett. 370, 215-221, 1995
A;Title: Expression of serotonin receptor mRNAs in blood vessels.
A;Reference number: S66487; MUID:95385798; PMID:7656980
A;Accession: S66493
A;Status: preliminary
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88.7%; Pred. No. 2.3e-152;
ive 11; Mismatches 18; Indels
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Matches 338; Conservative
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genome of the puffer fi
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Mol. Pharmacol. 150475
Mol. Pharmacol. 150475
Mol. Pharmacol. 150475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 LDRYYALCCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMGGWNN---IGIIDLERS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INQCLGQDFHAIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 AKEHAHQIQMLQRAGASSESRPQS-----ADQHSTHRM--RTETKAAKTLCIIMGCFCL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CWAPFFVINIVDPFIDYTVPG-----QVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dopamine receptor-like protein D14 - Japanese pufferfish
C;Species: Fugu rubripes (Japanese pufferfish)
C;Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                    C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDKLDANVSS--EEGFGSVEKVV-LLT--FLSTVILMAILGNLLVMVAVCWDRQLRKIKT
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A;Residues: 1-459 <MAC>
A;Zross-referances: GB:X80174; NID:g1204089; PIDN:CAA56455.1; PID:g1204090
C;Superfamily: vertebrate rhodopsin
C;Reywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L08602; NID:g212949; PIDN:AAA16322.1; PID:g212950
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.6%; Score 610; DB 2; Length 36 Best Local Similarity 38.4%; Pred. No. 1.8e-47; Matches 140; Conservative 65; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: A56849
R,Macrae, A.D.; Brenner, S.
Genomics 25, 436-446, 1995
A;Title: Analysis of the dopamine receptor family in the A;Reference number: A56849; WUID:95309911; PMID:7789977
A;Accession: A56849
A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                            dopamine D1 receptor - goldfish
C;Species: Carassius auratus (goldfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-363 <FRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for residue 440
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                                                                                                                                                                                                                                                                                                                                                                                                         183 AIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                      48 -IEKRKFHQNSNSTYCIFMYNKPYAITCSVVAFYIPFLLMVLAYWRIYVTAKEHAHQIQM 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CWVIPTFISFLPIMQGWN -- - NIGIIDLERSLNQGLGQDFHAIEKRKFNQNSNSTYCVFM 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NCDSS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GASS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESRPOSADOHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFIDYTVPGQ---- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 FCINSTIFDVFIWFGWANSSLNPIIYAF-NADFRKAFSTLLGC----YRLCPMSGNAI-- 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Demchyshyn, L.L.; Sugamori, K.S.; Lee, F.J.S.; Hamadanizadeh, S.A.; Niznik, Biol. Chem. 270, 4005-4012, 1995; Title: The dopamine DID receptor. Cloning and characterization of three phar
                                                                                                                                                                                                                                                                                                                                                         47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,Species: Galius gallus (chicken)
;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
;Accession: A55886
                  Status: preliminary; nucleic acid sequence not shown; Molecule type: mRNA; Molecule type: mRNA; Status: 1-137 <ULL>; Residues: 1-137 <ULL>; RESIDUES: 1-137 <ULL>; RESIDUES: 1-137 <ULL>; Superfemence: EMEL: 248175; NID:g984242; PIDN:CAA88198.1; PID:g984243; Superfamily: vertebrate rhodopsin; Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                 1 CCQPLVYRNKMTPLRVAVLLACCWAIPVLISFLPIMQGWNNIGITDL-----
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                                                                                                                                                                                                    Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQRA----
                                                                                                                                                                                                                                                       8; Indels
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30.4%; Score 648; DB 2;
Best Local Similarity 80.8%; Pred. No. 2.3e-51;
Matches 122; Conservative 7; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 STTTINGSTHVLRDAVECGGWESDCHPPATSP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 LORAGASSESRPOSADQHSTHRMRTETKAAK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 1-450 <DEM>
Cross-references: GB:L36877

Note: authors translated the codon MET for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: authors translated the codon helperfamily: vertebrate rhodopsin Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 36.4<sup>3</sup>
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
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dopamine DIA receptor - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Laid-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C;Accession: 151659
R;Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Niznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10336-10540, 1994
A;Title: DIA, DIB, and DIC dopamine receptors from Xenopus laevis.
A;Reference number: 151659; MUID:95024150; PMID:7937989
A;Accession: 151659
C;Superfamily: vertebrate chodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
                                         6
                                                                                                                                                                                                                                                                   38 KVACLMISVAWTLSVIISFIPVQLNW
                                                                                                                                                                                                                                                                                                                                               FGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAICCQPLVYRNKMTF 135
                                                                                                                                                                                    136 LRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIEKRKFNQNSNS 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLI 339
                                                                                                                                                                                                                                                                                                                                                                                                     248 ASSESRPO----SADOHSTHRM--RIEIKAAKTLCIIMGCFCLCWAPFFVTNIVDPFI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAIC 123
                                                                                                    20 SSKRVLTGCFLSLLIFFTLLGNTLVCVAVTKFRHLRSKVTNFFVISLAISDLLVAILVMP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 SVEKVVLLI------FLSTVILMAILGNILVMVAVCWDRQLRKIKTNYFIVSLA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 ------DRIMDNCDSSLNRTYAISSSLISFYIPVAIMIVTYTRIYRIAAKQIRRI
                                                                               SVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLAFADLLVSVLVMP
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                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DY-----TVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCC 343
                                     47;
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  Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.6%; Score 588.5; DB 2; Length 4
34.5%; Pred. No. 2e-45;
ive 64; Mismatches 150; Indels
                                       Indels
; Score 591.5; DB 2;
; Pred. No. 1.1e-45;
60; Mismatches 114;
  37.0%;
                                       130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 34.5
Matches 146; Conservative
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                    Similarity
Query Match
Best Local S
Matches 130
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A.Map position: 5934-5935
C.Superfamily: vertebrate rhodopsin
C.Superfamily: reassmembrane #status predicted <TM1>
F.51-87/Domain: transmembrane #status predicted <TM2>
F.51-13/Domain: transmembrane #status predicted <TM3>
F.14-14/Domain: transmembrane #status predicted <TM5>
F.14-23/Domain: transmembrane #status predicted <TM5>
F.215-273/Domain: transmembrane #status predicted <TM7>
F.215-273/Domain: transmembrane #status predicted <FTM7>
F.2175-S.268/Binding site: phosphate (Str) (covalent) #status predicted F.337/Rinding site: plosphate (Str) (covalent) #status predicted <FTM7+ S.259, 263/Binding site: phosphate (Str) (covalent) #status predicted
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A;Residues: 1-446 <ZHO>
A;Cross-references: EMBL:X58987
R;Dearry, A.; Gingrich, J.A.; Falardeau, P.; Fremeau Jr., R.T.; Bates, M.D.; Caron, Nature 347, 72-76, 1950
A;Tille: Molecular cloning and expression of the gene for a human D(1) dopamine rec A;Reference number: S11376; MUID:90370093; PMID:2144334
A;Accession: S11376
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A;Residues: 1-446 c.DEA.
A;Cross-references: EMBL:X55760; NID:g30396; PIDN:CAA39286.1; PID:g30397
A;Cross-references: EMBL:X55760; NID:g30396; PIDN:CAA39286.1; PID:g30397
R;Sunahara, R.K.; Niznik, H.B.; Weiner, D.M.; Stormann, T.M.; Brann, M.R.; Kennedy,
Nature 347, 80-83, 1990
A;Title: Human dopamine D11 receptor encoded by an intronless gene on chromosome 5
A;Reference number: S11379; MUID:90370095; PMID:1975640
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288 FILNCIVPFCDPSLITTSGTEPFCISSTTPDVFVWFGWANSSLNPIIYAF-NADFRKAFSN 346
                                                                                                                                                                      347 LLGC----YRLCPTSNNII--ETVSINNNGAVVYSCQQEPKGSIPNECNLVYLIPHAIIC 400
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                                                                                       340 ILCCDDERYRRPSILGQTVPCSTTTINGSTHVLRDA-VECGGOWESQCHPPATSPLVAAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Homo sapiens (man)
C; Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 22-Jun-19
C; Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 22-Jun-19
C; Accession: S11377; S11376; S11379
R; Zhou, O; V.Y.; Grandy, D.K.; Thambi, L.; Kushner, J.A.; van Tol, H.H.M.; C
Nature 347, 76-80, 1990
A; Title: Cloning and expression of human and rat D(1) dopamine receptors.
A; Reference number: S11377; MUID:90370094; PMID:2168520
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A;Molecule type: DNA
A;Residues: 1-446 <SUN>
A;Cross-references: GB:X55758; NID:g288931; PIDN:CAA39284.1; PID:g288932
C;Genetics:
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C;Species: Meleagris gallopavo (common turkey)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 13-Aug-1999
C;Accession: A25896
                                                                                                   C.Species: Xenopus laevis (African clawed frog)
C.Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text_change 13-Aug-1999
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R,Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Niznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A;Title: D1A, D1B, and D1C dopamine receptors from Xenopus lacvis.
A;Teterence number: IS1659; MUID:95024150; PMID:7937989
A,Accession: IS1661
A;Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A;Residues: 1-465 <SUG>A;Residues: 1-465 <SUG>A;Conse-reference EMBL:U07865; NID:9559763; PIDN:AAA50830.1; PID:9559764
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
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A;Cross-references: GB:M14379; NID:g213891; PIDN:AAA49627.1; PID:g213892
A;Experimental source: erythrocyte
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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A.Jitle: The avian Sci. act-adrenergic receptor: primary structure and A.Reference number: A25896; MUID:86313664; PMID:3018746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.2%; Score 580; DB 2; Length 46
Best Local Similarity 39.0%; Pred. No. 1.2e-44;
Matches 130; Conservative 53; Migmatches 114; Indels
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                                                                             (fragment)
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dopamine DIC receptor - African clawed frog (fi
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m. J. Physiol. 268, F423-F434, 1995
m. J. Physiol. 268, F423-F434, 1995
j'Title: Cloning of the porcine D1A dopamine receptor gene expressed in renal epithelial
Reference number: I47217; MUID:95208810; PMID:7900842
Accession: I47217
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                              ----AKPTSPSDGNATSLAETIDNCDSSLSRTYAISSSVISFYIPVAIMIVTYTRIYRIA 221
                                                                                                                                                                                                                                             GCFCLCWAPFFVTNIVDPF1-----DYTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSF 333
                                                                                                                                                                                                                                                                                                                                              279 GVFVCCWLPFFILNCILPFCGSGETQPFCIDSNTFDVFVWFGWANSLNPIIYAF-NADF 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLAVSDLLVAVLVMPWKAVAEIAGFWPFGS-FCNIWVAFDIMCSTASILNLCVISVDRYW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AICCOPLVYRNIGHTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AICCOPLVYRNKWTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLBRSLNQGLGOD 180
                                                                                                         181 FHAIEKRKFNONSNST-----YCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTA 233
                                                                                                                                                                                                               234 KEHAHQIQMLQRAGASSE......SRPQSADQHSTHRMRTETKAAKTLCIIM 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 NVSSEEGFGSVE-----KVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opamine receptor - pig
;Species: Sus scrofa domestica (domestic pig)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHAIBKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:U25681; NID:9808097; PIDN:AAA79848.1; PID:9808098
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                                                                                                                                                                                                                                                                                                                                                                                                                            RRAFLIILCCDDERYRRPSILGQTVPCSTTTING-----STHVLRDAV--EC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| :| | | : | | | 338 RKAFSTLIGC----YRLCPATNNAIETVSINNNGAAMFSSHHEPRGSISKEC 385
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33.9%; Pred. No. 8.6e-45;
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Molecule type: DNA;
Residues: 1-446 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: D1A
Superfamily: vertebrate rhodopsin
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Best Local Similarity
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CCISLDRYYA CVIALDRYLA SLNOGLGODE SLNOGLGODE TAKEHAHQIQ EAKEQIRKID SLIMGCFCLC SLIMGCFCLC AFLILLCCDD	QY 265 -MRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFIDYTVPGQVWTAFIWLGYI 317
	umber: A56849; MUID:95309911; FMID:7789977 B56849
S72168 dopamine receptor D1C - Mozambique tilapia dopamine receptor D1C - Mozambique tilapia C;Species: Tilapia mossambica, Oreochromis mossambicus (Mozambique tilapia) C;Species: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 13-Aug-1999 C;Accession: S72168; S51675 S;Lamers, A.E.; Groeneveld, D.; de Kleijn, D.P.V.; Geeraedts, P.C.G.; Leunissen, J.A.M.; Biochim. Biophys. Acra 1308, 17-22, 1996 A;Title: Cloning and sequence analysis of a hypothalamic cDNA encoding a D(1c) dopamine	Query Match 26.6%; Score 568; DB 2; Length 463; Best Local Similarity 34.3%; Pred. No. 1.5e-43; Matches 138; Conservative 57; Mismatches 131; Indels 76; Gaps 26 LSTVILMALIGNLLWWVAVCWDRQLRKIKINYFIVSLAFADLLVSVLVWPFGAIELVQDI
A; Keererene number: S/2168; MulD:96328259; PMID:8765745 A; Accession: S72168 A; Molecule type: mRNA A; Residues: 1-386 < LAM> A; Residues: 1-386 < LAM> C; Superferences: EMBL:X81969; NID:9603868; PIDN:CAA57494.1; PID:9603869 C; Superfamily: vertebrate rhodopsin C; Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter rece F; 34-59/Domain: transmembrane #status predicted <tm1> F; 110-111/Domain: transmembrane #status predicted <tm2> F; 110-111/Domain: transmembrane #status predicted <tm3> F; 110-111/Domain: transmembrane #status predicted <tm3></tm3></tm3></tm2></tm1>	OY B6 WYGRYCLVRTSLDLTTABIFHLCISLDRYALCCQFLYRAWPERIAMMLGGC 145
Filto-12/14/Domain: transmembrane #status predicted <tms> Fil53-174/Domain: transmembrane #status predicted <tms> Fil56-217/Domain: transmembrane #status predicted <tms> Fil56-225/Domain: transmembrane #status predicted <tms> Fil66-225/Domain: transmembrane #status predicted <tms> Fil69-25/Domain: transmembrane #status predicted <tms> Fil48,261/Binding site: phosphate (Thr) (covalent) #status predicted Fil21,252,256/Binding site: phosphate (Ser) (covalent) #status predicted Fil69-25/Binding site: palmitate (Cys) (covalent) #status predicted Fil69-25/Binding site: palmitate (Cys) (covalent) #status predicted</tms></tms></tms></tms></tms></tms>	Db 198 INRTYAISSLISTIT
Db 102 WEG-Decorated SINITIATING SHORT SHO	Oy 370 HVLRDAVECGGOWESQCHP
QY 146 WVIPTFISFLPIMGGMNNIGIIDLERSLNQGLGQDFHAIEKRKFNQNSNSTYCVFMVNKP 205	

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rattus norv
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    protein search, using sw model

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TAR1 RAT	B2AR_HUMAN	TAR1 MACMU	HHZR HUMAN	HH2R PANTR	BlAR PIG	SHT1 APLCA	B2AR PIG	B2AR FELCA	TAR1 MOUSE	B4AR_MELGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=013639-7; Sequence=VSP 001850; TISSUE SPECIFICITY: Isoform 5-HT4(A) is expressed in ileum, brain, and atrium, but not in the ventricle. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                 Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
"Expression of sercotonin receptor mRNAs in Diood vessels.";
"Expression of sercotonin receptor mRNAs in Diood vessels.";
FEBS Lett., 370:215-221 (1995).
-1- FUNCTION: This is one of the several different receptors for 5-
hydroxytryptamine (sercotonin), a biogenic hormone that functions as neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylate
                                                                     벙
                          MEDLINE=20110418; PubMed=10646498; Bang Y.B., Gommeren W., Bender E., Pindon A., van Oers I., Zhang Y.B., Gommeren W., Verhasselt P., Jurzak W., Leysen J., Luyten W.; "Structure of the human serotonin 5-HT4 receptor gene and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO: GO:0005887; C:integral to plasma membrane; TAS.
GO: GO:0004993; F:serotonin receptor activity; TAS.
GO: GO:0007187; P:G-protein signaling, coupled to cyclic nucl.
InterPro; IPR00276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                              SÜBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist;
Name=5-HT4(B);
             OF 10-388 FROM N.A. (ISOFORM 5-HT4(F))
                                                                                                                                                                                                                                                                                                                                                                 Name=5-HT4(A); Synonyms=5-HT4S;
IsoId=Q13639-2; Sequence=VSP_001849;
                                                                                                                                                                                                                                                                                                                                                                                                          Isold=013639-3; Sequence=VSP_001848;
Name=5-HT4(D);
Isold=013639-4; Sequence=VSP_001847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=5-HT4(E); Synonyms=H5-HT4(g);
IsoId=013639-5; Sequence=VSP_001846;
Name=5-HT4(F);
IsoId=013639-6; Sequence=VSP_001845;
                                                                                                                                                                                                                                                                                                                                                     IsoId=013639-1; Sequence=Displayed;
                                                                                                                                                      MEDLINE=95385798; PubMed=7656980;
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EMBL; Y12505; CAA73108.1; -...
EMBL; Y12507; CAA73108.1; -...
EMBL; Y10437; CAA71462.1; -...
EMBL; Y09586; CAA70002.1; -...
EMBL; Y09586; CAA70002.1; -...
EMBL; X013584; CAA7931.1; -...
EMBL; AJ21313; CAB71316.1; -...
EMBL; AJ278979; CAC22248.1; -...
EMBL; AJ278979; CAC22250.1; -...
EMBL; AJ278979; CAC22250.1; -...
EMBL; Z48150; CAA88167.1; -...
EMBL; Z48150; CAA88167.1; -...
EMBL; S66493; S66493.
HSSP; P29274; 1MMH; Genew; HGNC; 2299; HTR4.
                                                                               novel 5-HT4 splice variant.";
J. Neurochem. 74:478-489(2000)
                                                                                                                        SEQUENCE OF 112-255 FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00001; 7tm 1; 1. PRINTS; PR00237; GPCRRHODOPSN
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                                                                                                                                                                                                                                                                                                                                                                    RDAVECGGGWESQCHPPATSPLVAAQPSDT -> SGCSPVS
SPELLECNEWPYPVPV (in isoform 5-HT4(E)).
FTIG-USP 001846.
RDAVECGGGWESQCHPPATSPLVAAQPSDT -> SSGTETD
MENGTREKRITKPS (in isoform 5-HT4(D)).
FTIG-USP 001847.
DAVECGGWESQCHPPATSPLVAAQPSDT -> F (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMLORAGASSESRPOSADOHSTHRMRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 QMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDROLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDKLDANVSSEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCHDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AICCOPLVYRNKMTPLRIALMLGGGWVIPTFISFLPIMGGWNNIGIIDLERSLNQGLGOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHAI EKRKFNONSNSTYCVFMVNKPYAI TCSVVAFYI PFLLLMVLAYYR I YVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYKRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTVPGQVWTAPLWLGYINSGLNPPLYAPLNKSFRRAFLIILCCDDERYRRPSILGQTVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                BY SIMILARITY.
S-palmitoyl cysteine (By similarity)
                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINNED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
 G_PROTEIN_RECEP_Fl_1; 1.
G_PROTEIN_RECEP_Fl_2; 1.
receptor; Transmembrane; Glycoprotein;
Lipoprotein; Palmitate; Alternative splicing.
Lipoprotein; Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                            L -> LERSINQGIGQDFHA (in isoform 5-HT4(F)).
/FTId=VSP_001845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAVECGGOWESOCHPPATSPLVAAQPSDT ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.7%; Score 2042; DB 1; Length 388; 96.5%; Pred. No. 1.2e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FIId=VSP 001849.
Missing (in isoform 5-HT4(G)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                              3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VSP 001850.
7FCFEC60E7BDF560 CRC64;
                                                                                                                                                                                           5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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/FT1d=VSP_001848.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 AA; 43761 MW;
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Matches 300; Conservative
                                                             184
329
169
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PROSITE; PS00237; G
PROSITE; PS50262; G
G-protein coupled ri
Multigene family; L.
DOMAIN 20
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TRANSMEM
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DISULFID
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                                                                                                                                                                                                                                                                     DOMAIN
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Pred. No. 3.5e-136;
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                          8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97102706; PubMed=8946946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD; PR
O89004; Q9R2A4;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Swiss, TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 398:19-25(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Swise;
                            Matches 370;
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5H4_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

FUNCTION: This is one of the several different receptors for 5-
FUNCTION: This is one of the several different receptors for 5-
FUNCTION: This is one of the several different receptors as as a neurotransmitter, a bormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylate cyclase (By similarity).

AUTERNATIVE RODUCTS:

EVENT.ALLUR PRODUCTS:

EVENT.ALLUR DICT. Named isoforms=1;

COMMENT.ALLUR DICT. STILL ST
                                                                                                                                                                                                                                                                                                                                                                                                                             Van den Wyngaert I., Gommeren W., Jurzak M., Verhasselt P., Gordon R.
                                                                                                                                                                                                                              (Serotonin receptor) (5-HT4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isold=070528-1; Sequence=Displayed;
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                  Craniata, Vertebrata, Buteleostomi,
Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  palmitoyl cysteine (By similarity)
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leysen J., Luyten W., Bender E.; "Cloning and expression of 5-HT4 receptor species and splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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7 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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(POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                            JO-TMI-2000 (Rel. 39, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) 5-hydroxytryptamine 4 receptor (5-HT-4) (Seroi HTR4.
                                                                                                      388 AA
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                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                  (Rel. 39, Created)
(Rel. 39, Last seq
(Rel. 42, Last ann
                                                                                                                                                                                                                                                                          Cavía porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ
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HSSP; P29274; IMMH.
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                                                                                                   STANDARD;
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739
739
1116
1137
1192
2113
2291
3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variants.";
Submitted (JUN-1997)
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                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10141;
                                                                                                                                                     30-MAY-2000
                                                                                                5H4 CAVPO
070528;
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DOMAIN
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                                                 ESULT 2
H4_CAVPO
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91.6%; Score 1954; DB 1; Length 388;

Query Match

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                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                                                                                                                          OMLORAGASSESRPOSADOHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                              SLAFADLLVSVLVMPFGAIBLVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                                                                                                 121 AICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                       YTVPGOVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
                                                                           9
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MEDLINE=99238795; PubMed=10220570;
Clackgen B., Sebben M., Becamel C., Bockaert J., Dumuis A.;
Novel brain-specific 5-HT4 receptor splice variants show marked constitutive activity: role of the C-terminal intracellular domain.";
Mol. Pharmacol. 55:910-920(1999).
                                                            1 MDKLDANVSSKEGFGSVEKVVLLTFLSAVILMAILGNLLVMVAVCKDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHARQI
                                                                                                                                           SLAFADILLVSVLVMPFGAIELVQDIWVYGEMFCLVRTSLDVLLTTASIFHLCCISLDRYY
                                     1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                            PHAIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P97288; 089003; 089004; Q9R2A4;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
5-bydroxytryptamine 4 receptor (5-HT-4) (Serotonin receptor) (5-HT4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99127199; PubMed=9928218;
Clasysen S., Faye P., Sebben M., Taviaux S., Bockaert J., Dumuis A.;
S-HT4 receptors: cloning and expression of new splice variants.";
Ann. N.Y. Acad. Sci. 861:49-56(1998).
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: This is one of the several different receptors for 5-
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claeysen S., Sebben M., Journot L., Bockaert J., Dumuis A.; "Cloning, expression and pharmacology of the mouse 5-HT(4L) receptor.";
Indels
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STTTINGSTHVLRDTVECGGQWESQCHPAASSPLVAAQPIDT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A) AND 5-HT4(E))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STITINGSTHVLRDAVECGGQWESQCHPPATSPLVAAQPSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-palmitoyl cysteine (By similarity).
DAVECGGOWESRCHLTATSPLVAAQPSDT -> YTVLHSGH
HQELEKLPIHNDPESLESCF (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDAVECGGOWESRCHLTATSPLVAAQPSDT -> SFPLLFR
NRPVPV (in isoform 5-HT4(E)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAVECGGOWESRCHLTATSPLVAAQPSDT -> PVPV (in
        as a neurotransmitter, a hormone, and amitogen. The activity of this receptor is mediated by G proteins that stimulates adenylate cyclase (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
hydroxytryptamine (serotonin), a biogenic hormone that functions
                                                                                                                                                                   Name=5-HT4(F);
IsoId=P972884; Sequence=VSP 001853;
SIMILARITY: Belongs to family I of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:109246; Htr4.
InterPro; IPR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODDSN.
PROSITE; PS00237; GFCRHODDSN.
PROSITE; PS50262; GFROTEIN RECEP_F1_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Lippprotein; Palmitate; Alternative splicing.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 (POTENTIAL).
EXTRACELLUAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform 5-HT4(F)) /FIId=VSP_001853.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                  Name=5-HT4(A);
Isold=P97288-2; Sequence=VSP_001851;
                                                                                                                                            Name=5-HT4(E);
Isold=P97288-3; Sequence=VSP_001852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                       IsoId=P97288-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                 YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPC 360
                                                                                                                                                                                                                                                                                                                                                                 YTVPEQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYKRPPILGQTVPC 346
                     9
MEDLINE-99238795; PubMed-10220570; Clasysen S., Sebben M., Becamel C., Bockaert J., Dumuis A.; Clasysen S., Sebben M., Becamel C., Bockaert J., Dumuis A.; Clasysen S., Sebben M., Becamel C., Ecaptor splice variants show marked "Novel brain-specific 5-HT4 receptor splice variants show marked constitutive activity: role of the C-terminal intracellular domain."; Mol. Pharmacol. 55:910-920(1999).

-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylate
                                                                                                                                           181 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                              ---IEKRKFSHNSNSTWCVFMVNKPYAITCSVVAFYIPFLLMVLAYKIYVTAKEHAQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95317299; PubMed=7796807;
MEDLINE=95317299; PubMed=7796807;
Gerald C., Adham N., Kao H.T., Olsen M.A., Laz T.M., Schechter L.E.,
Bard J.A., Vaysse P., Hartig P.R., Parachek T.A., Weinshank R.L.;
"The 5-HT4 receptor: molecular cloning and pharmacological
"The reretrization of two splice variants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5H4_RAT STANDARD; PRT; 406 AA.
062758; 089034; Q62757; Q63006;
01-NVV-1997 (Rel. 35, Created)
10-NVV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 4 receptor (5-HT-4) (Serotonin receptor) (5-HT4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95385798; PubMed-7656980;
Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
"Expression of serotonin receptor mRNAs in blood vessels.";
FEBS Lett, 370:215-221(1995).
                                                                                                                                                                                                                                                                                                                                                                                                       402
                                                                                                                                                                                                                                                                                                                                                                                                                       SÜBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                     STITINGSTHVLRDAVECGGOWESQCHPPATSPLVAAQPSDT
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; Score 1913; DB 1; Length 388; ; Pred. No. 3.5e-133; 11; Mismatches 14; Indels 14;

89.7**%**; 90.3**%**;

Matches 363; Conservative

Similarity

Query Match Best Local Ŋ

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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
S-palmitoyl cysteine (By similarity).
DYDEGGGGGRESCHLARISPLAAQPYIRRPODNDLEDSCS.
LYRSGS -> YTVLHSGQHQELEKLPIHNDPESLESCF.
(in isoform S-HT4S).
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RDTVECGGQWESRCHLTATSPLVAAQPVIRRPQDNDLEDSC
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R BEBL; U20906; AAC52233.1; -
R EMBL; U20906; AAC52233.1; -
R EMBL; A201370; CAA09599.1; -
R EMBL; A2010276; GPCR Rhodpsn.
R HSSP, P29274; IMM.
R PROSITE; PS00237; GPCREIN RECEP.F1.1; 1.
R PROSITE; PS00237; GPCREIN RECEP.F1.2; 1.
TRANSKEM 20 40 1 (POTENTIAL).
T TRANSKEM 30 79 2 (POTENTIAL).
T TRANSKEM 34 116 3 (POTENTIAL).
T TRANSKEM 138 158 4 (POTENTIAL).
T TRANSKEM 138 158 4 (POTENTIAL).
T TRANSKEM 138 158 6 (POTENTIAL).
T TRANSKEM 261 294 EXTRACELLULAR (POTENTIAL).
T TRANSKEM 261 294 TEXTRACELLULAR (POTENTIAL).
                                                                                                                                                                              TISSUE SPECIFICITY: In brain, the 5-HT4S transcripts are TISSUE SPECIFICITY: In brain, the 5-HT4S transcripts are restricted to the striatum, but the 5-HT4L transcripts are expessed throughout the brain, except in the cerebellum. In peripheral tissues, differential expression is also observed in the arrium of the heart where only the 5-HT4S isoform is detectable. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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NA -> MP (IN REF. 3).
A1889155A08930B4 CRC64;
Comment=Additional isoforms seem to exist;
                                                                                                                      Isold=Q62758-2; Sequence=VSP_001854;
Name=5-HT4(E);
                          Name=5-HT4L;
IsoId=Q62758-1; Sequence=Displayed;
Name=5-HT4S;
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406 AA;
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CARBOHYD
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-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SIMILARITY: Belongs to family 1 of 6-protein coupled receptors. Sus scrofa (Pig). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus. EMBL; Z48175; CAA88198.1; -.

INT. S66487; S66487.

InterPro; IRPO00276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm.1; 1.

PRINTS; PF00237; GPCRENDONSN.

PROSITE; PS00237; GPCREND RECEP_F1.1; PARTIAL.

PROSITE; PS0262; G_PROTEIN_RECEP_F1.2; 1.

Multigene family.

1 STITINGSTHVLRDAVECGGGWESQCHPPATSPLVAAOP Ź 137 PRT; STANDARD; (Fragment). 287 61 170 241 227 301 361 347 61 121 5H4 PIG Q29006; RESULT 5 5H4_PIG 셤 8 8 셤 8 셤 ઠે 쉱 ሯ ద 8 ઠ

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb.sib.ch).
                                                                                                                                                                                                        123 CCQPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFH 182
                                                                                                                                                                                                                                                                             183 AIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQM 242
                                                                                                                                                                                                                                                                                               48 -IEKRKFHQNSNSTYCIFMVNKPYAITCSVVAPYIPFLLMVLAYWRIYVTAKEHAHQIQM 106
                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from goldfish retina: stimulation of a truncated dopamine D1 receptor from goldfish retina: stimulation of cyclic AMP production and calcium mobilization.";

Mol. pharmacol. 44:1113-1118(1993).

-!- FUNCTION: This is one of the five types (D1 to D5) of receptors for dopamine. the activity of this receptor is mediated by G proteins which activate adenylyl cyclase. Could be involved in growth hormone release.

-!- SUBCELLUIAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94088471; Pubmed=8264547;
Frail D.E., Manelli A.M., Witte D.G., Lin C.W., Steffey M.E.,
MacKenzie R.G.;
                                                                                                                                     Length 137;
                                                                                                                                                                                                                              CCQPLVYRNKMTPLRVAVLLAGCWAIPVLISFLPIMQGWNNIGITDL-
                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0237; GFCRHODDSN.
PROSITE; PS00237; GFCRHODDSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS02625, G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
                  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                   137 AA; 15622 MW; C9D60744DA4D0263 CRC64;
                                                5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                     Score 648; DB 1;
Pred. No. 5.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  LORAGASSESRPOSADQHSTHRMRTETKAAK 273
                                                                                                                                                                                                                                                                                                                                                                                  LORAGAPAEGRPPSADOHSTHRMRTETKAAK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AA
                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carassius auratus (Goldfish).
                                                                                                                                    30.4%;
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PIR; I50475; I50475.
                                                                                                                                                                        Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00001, 7tm 1, 1.
 15
36
70
91
*137
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                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994
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                                  DOMAIN
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DOMAIN
TRANSMEM
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                                                                                                   SEQUENCE
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P35406;
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61 NFFVISLAVSDLLVAVLVMPWKAVTEVAGFWPFG-AFCDIWVAFDIMCSTASILNLCVIS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 CWLPPFILNCMVPFCKRISNCLPCISPTTFDVFVWFGWANSSLNPIIYAP-NADFRRAFA 340
                                                                                                                                                                                                                                                                                                                                                                                                       56 NYFIVSLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCIS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 LDRYYAICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMOGWNN---IGIIDLERS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 LNQGLQQDFHAIBKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AKEHAHQIQMLQRAGASSESRPQS-----ADQHSTHRM--RTETKAAKTLCIIMGCFCL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CWAPFFVINIVDPFIDYTVPG-----QVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 AOKOIRRÍSALERAAESAOIRHDSMGSGSNMÓLESSFKLSFKRETKVLKTLSVÍMGVFVC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAVLDLNLTTVIDSGFMESDRSVRVLTGCFLSVLILSTLLGNTLVCAAVTKFRHLRSKVT
                                                                                                                                                                                                                                                                                                                                              1 MDKLDANVSS--EEGFGSVEKVV-LLT--FLSTVILMAILGNLLVMVAVCWDRQLRKIKT
                                                                                                                                                                                                                                                                                                                    42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pugu rubripes (Japanese pufferfish).(Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostcmi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95309911; PubMed=7789977;
Machae A.D., Brenner S.;
"Analysis of the dopamine receptor family in the compact genome of
                                                                                                                                                                                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
S-palnitoyl cysteine (By similarity)
4847FDE240D65DD0 CRC64;
                                                                                                                                                                                                                                                                                        Length 363;
                                                                                                                                                                                                                                                                                                                 65; Mismatches 118; Indels
                                                                                                                           5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                     3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                      EXTRACELLULAR (POTENTIAL)
                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                      28.6%; Score 610; DB 1; 38.4%; Pred. No. 8.4e-38;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last seq 01-0CT-1996 (Rel. 34, Last ann D(1)-like dopamine receptor.
                                                                                                                                                                                                                                                           40651 MW;
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 140; Conserv
                                                                                                                                                                                                                                                             363 AA;
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                                                                                  DOMAIN
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TRANSMEM
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                            DOMAIN
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TRANSMEM
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             RANSMEM
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DIDR_FUGRU
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11;

25 9 us-10-018-257a-2.rsp

451 AA.

STANDARD;

XENLA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 FGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAICCOPLVYRNKMTP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 LRIALMIGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGIGQDFHAIEKRKFNQNSNS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TY-----CVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQRAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 ASSESRPQ----SADQHSTHRM--RTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 SSKRVLTGCFLSLLIFTTLLGNTLVCVAVTKFRHLRSKVTNFFVISLAISDLLVAILVMP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVEKVVLLIFLSTVILMAILGNILVMVAVCWDRQLRKIKTNYFIVSLAFADLLVSVLVMP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
            Genomics 25:436-446(1995).
-1- FUNCTION: Receptor for dopamine.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DY-----TVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.7%; Score 591.5; DB 1; Length 4: 37.0%; Pred. No. 2.4e-36; ive 60; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                              InterPro; IRR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1 2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1 2; 1.

Rulligene family.
DOMAIN

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z (FOIENIIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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fish Fugu rubripes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51080 MW;
                                                                                                                                                                                                                                                                            EMBL; X80174; CAA56455.1; -. PIR; A56849; A56849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 AA;
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DOMAIN
TRANSMEM
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TRANSMEM
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TRANSMEM
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DISULFID
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TRANSMEM
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Best Local
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Matches
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ADR_XENLA ESULT 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDLLVAVLVMPWKAVAEIAGFWPFG-TFCNIWVAFDIMCSTASILNLCVISVDRYWAI- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 PADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SMDEDVILIERESSFRVLTGCFLSVLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVISLA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVEKVVLLT------FLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Gaps
                                                                                                                                                                                                                                      Sugamori K.S., Demchyshyn L.L., Chung M., Niznik H.B.;
"DlA, DlB, and DlC dopamine receptors from Xenopus laevis.";
Proc. Natl. Acad. Sci. U.S.A. 91:10536-10540(1994)
-!- FUNCTION: This is one of the five types (Dl to D5) of receptors
for dopamine. The activity of this receptor is mediated by G
proteins which activate adenylyl cyclase.
-- SUBCELLULAR LOCATION: Integral membrane protein.
-- TISSUB SPECIFICITY: Brain.
-- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                               D(1A) dopamine receptor.
Stanopus laevis (African clawed frog).
Sukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-palmitoyl cysteine (By similarity) 3A0F8AB36C166687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS: PRODOCATE GPCR_Rhodpsn.

PRINTS: PRO0237; GPCRRHODDSN.

PROSITE; PS00237; GPCRRHODDSN.

PROSITE; PS00237; GPROTEIN RECEP P1 1; 1.

PROSITE; PS00262; G_PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.

DOMAIN 1 22 EXTRACRILLINAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.6%; Score 588.5; DB 1; Length 34.5%; Pred. No. 3.8e-36; Live 64; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (POTENTIAL),
CYTOPLASMIC (POTENTIAL),
2 (POTENTIAL),
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=95024150; Pubmed=7937989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50549 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U07863; AAA50828.1; -.
PIR; I51659; I51659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                    Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                     NCBI_TaxID=8355;
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Matches 146;
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Local Similarity
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                                                                                                                                                                                                                                                                                  FVINIVDPFID-----YTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLI 339
  COPLVYRNKWTFLRIALMLGGCWVIPTFISFLPIMOGWN---NIGIIDLERSLNOGLGOD 180
                                                                                                                                                                                                                                                                                                                                               340 ILCCDDERYRRPSILGQTVPCSTTTINGSTHVLRDA-VECGGQWESQCHPPATSPLVAAQ 398
                                                                                                                                                                                                                                                                                                                                                                                    LLGC----YRLCPTSNNII--ETVSİNNNGAVVYSCQQEPKGSIPNECNLVYLIPHAIIC 400
                                                                                                             241 QMLQRAGA-----SSESRPQSAD-QHSTHRMRT----BTKAAKTLCIIMGCFCLCWAPF
                                                                                                                                                                                                181 FHAIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nash S.R., Godinot N., Caron M.G., Cloning and characterization of the opossum kidney cell D1 dopamine receptor: expression of identical D1A and D1B dopamine receptor mRNAs in opossum kidney and brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Pharmacol. 44:918-925(1993).

-!- FUNCTION: This is one of the five types (D1 to D5) of receptors for dopamine. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Didelphis marsupialis virginiana (North American opossum).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
                                          SSPERYERKMTPKVAFIMIGVAWTLSVLÍSFIPVOLNWHKAKTTSFFDLNITLH-
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InterPro; IPR00276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00037; GPCRHODDSN.
PROSITE; PS00237; GPCRHODDSN.
PROSITE; PS01267; GPROTEIN RECREPF1 1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
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MEDLINE=94067048; PubMed=8246914;
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10-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caron M.G.;
Wolecular cloning and expression of the gene for a human D1 dopamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dearry A., Gingrich J.A., Falardeau P., Fremeau R.T. Jr., Bates M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Gaps
                                                                                                                                                       6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

BY SIMILARITY.

S-palmicoyl cysteine (By similarity).

S-palmicoyl cysteine (By similarity).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                            27.5%; Score 587; DB 1; Length 446; 34.8%; Pred. No. 4.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                          69; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                 49761 MW. AGBIFF3CBFE6476C CRC64;
                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
EXTRACELLULÂR (POTENTIAL)
                          3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                 5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 143; Conservative
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Brann M.R.,

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Neuropsychopharmacology 8:131-135(1993).
[5]
SEQUENCE FROM N.A.
Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=93228762; PubMed=8471124;
Ohara K., Ulpian C., Seeman P., Sunahara R.K., van Tol H.H.M.,
Niznik H.B.;
"Schizophrenia: dopamine D1 receptor sequence is normal, but has DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integrál membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                        Zhou Q.-Y., Grandy D.K., Thambi L., Kushner J.A., van Tol H.H.M., Cone R., Pribnow D., Salon J., Bunzow J.R., Civelli O., "Cloning and expression of human and rat Dl dopamine receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purl H.L. III, Ikeda S.R., Aronstam R.S., signal transduction "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 MEDLINE=90370095; PubMed=1975640;
Sunahara R.K., Niznik H.B., Weiner D.M., Stormann T.M., Brann
Kennedy J.L., Gelernter J.E., Rozmahel R., Yang Y., Israel Y.
Seeman P., OʻDowd B.F.;
"Human dopamine D1 receptor encoded by an intronless gene on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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MEDLINE=20086865; PubMed=10618483;
MEDLINE=90370094; PubMed=2168520;
                                                                                                                 Nature 347:76-80(1990).
                                                                                                                                                                                                                                                                                                                                                                                Nature 347:80-83(1990)
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SEQUENCE FROM N.A.
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; 126449; -. GO:0005623; C:cell; TAS.
GO:0005682; C:integral to plasma membrane; TAS.
GO:0004952; F:dopamine receptor activity; TAS.
GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO:0007212; P:dopamine receptor signaling pathway; TAS. EMEL; 558541; AABZ6273.1; -EMEL; AB06567; BAC65902.1; -EMEL; AP498961; AAM18131.1; -PIR; S11377; DYHUD1.
Genew; HGNC:3020; DRD1.
MIM; 126449; -GO; GO:0005687; C:cell; TAS.
GO; GO:0005687; C:integral to pl
GO; GO:0005245; F:dopamine recep
GO; GO:0007212; P:dopamine recep
GO; GO:0007212; P:dopamine recep EMBL; X55758; CAA39284.1; -. EMBL; X55760; CAA39286.1; -. EMBL; X58987; CAA41734.1; -.

12; 191 FHAIEKRKFNQNSNST----YCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTA 233 222 QKQIRRIAALERAAVHAKNCQTTTGNGKPVECSQPESSFKMSFKR---ETKVLKTLSVIM 278 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120 121 AICCOPLUYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180 279 GVFVCCWLPFFILNCILPFCGSGETQPFCIDSNTFDVFVWFGWANSSLNPIIYAF-NADF 337 9 64 7 NVSSEEGFGSV-----EKVVILTFLSTVILMAILGNLLVMVAVCWDROLRKIKTNYFIV 65 SLAVSDLLVAVLVMPWKAVAEIAGFWPFGS-FCNIWVAFDIMCSTASILNLCVISVDRYW 234 KEHAHOIOMLORAGASSE-----SRPOSADOHSTHRMRTETKAAKTLCIIM GCFCLCWAPFFVTNIVDPFI-----DYTVPGQVWTAFLWLGYINSGLNPFLYAFLNKSF NTSAMDGTGLVVERDFSVRILTACFLSLLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVI 71; Gaps R GO; GO:0007191; P:dopamine receptor, adenylate cyclase activa...; GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl...; R GO:0007268; P:G-protein signaling, coupled to cyclic nucl...; R InterPro; IPR00026; GPRCR.Rhodpsn...
R PRINTS; PR00237; GPCRHODDPSN.
R PROSITE; PS00237; GPRCTEIN RECEP F1 1; 1. G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family: Lipoprotein; Palmitate; Polymorphism. DOMAIN
TRANSMEM 24 49 I (POTENTIAL).
TRANSMEM 24 49 I (POTENTIAL).
TRANSMEM 50 60 CYTOPLASNIC (POTENTIAL).
TRANSMEM 61 87 (POTENTIAL). RRAFLILLCCDDERYRRPSILGQTVPCSTTTING----STHVLRDAV--EC 378 EXIMALLAL...
7 (POTENTIAL).
CYTOPLASMIC (BOTENTIAL).
N-T.INKED (GLCNAC. . .) (POTENTIAL) RKAFSTLLGC----YRLCPATNNAIETVSINNNGAAMFSSHHEPRGSISKEC 27.3%; Score 582.5; DB 1; Length 446; 33.7%; Pred. No. 1e-35; Indels 1 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 6 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 64E062D765D0DBA7 CRC64; /FTId=vAR 014671. R -> S (in dbSNP:5330). /FTId=vAR 014672. S -> A (in dbSNP:5331). /FTId=vAR 014673. I -> M (IN REF. 2). /FTId=VAR_014670. T -> R (in dbSNP:5328). (in dbsNP:5327). S-palmitoyl cysteine. S-palmitoyl cysteine. 67; Mismatches 135; م م 49293 MW; Best Local Similarity 33.79 Matches 139; Conservative 199 37 446 AA; Similarity 199 37 20 438 DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM CONFLICT ß 61 280 334 338 166 DISULFID Query Match CARBOHYD Local VARIANT **JARIANT JARIANT JARIANT** DOMAIN 쉱 g 8 g ð 셤 ઠે 쉱 8 ð 유 ò 유 à

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.3%; Score 581.5; DB 1; Length 446;
33.9%; Pred. No. 1.2e-35;
cive 64; Mismatches 146; Indels 63; Gaps
                                                                                                                                                                                                                             Grenader A.C., O'Rourke D.A., Healy D.P.; "Cloning of the porcine D1A dopamine receptor gene expressed in renal
                                                                                                                                                                                                                                                       epithelial LLC-PK1 cells.";
Am. J. Physiol. 268:P423-F434(1995).
-!- FUNCTION: This is one of the five types (D1 to D5) of receptors for dopamine. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.
-!- SUBUNT: Interacts with calcyon (By similarity).
-!- SUBCELLUMAR LOCATION: Integral membrane protein.
-!- SUBCELLUMAR LOCATION: Integral membrane protein.
                                                                                                                                      Eukaryota; Metāzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-palmitoyl cysteine (By similarity)
S-palmitoyl cysteine (By similarity)
A56BFA0D9JD50DBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.

SYSTALLARID.
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PRINTS; PR00237; GPCRRHODDSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50202; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                       (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
                             446 AA.
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                             PRT;
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=95208810; PubMed=7900842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49257 MW;
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                             STANDARD;
                                                                                                  D(1A) dopamine receptor.
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96
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312
337
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446 AA;
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                                                                                                                              Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273
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                                                        01-OCT-1996
                                                                    01-OCT-1996
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TRANSMEM
DOMAIN
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TRANSMEM
                             DADR PIG
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Best Local
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RESULT 11
DADR_PIG
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5 NTSTMDGTGLVVERDFSFRILTACPLSLLILSTLIGNTLVCAAVIRFRHLRSKVTNFFVI 64

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                                                                                                                                                                                                                                                                                                                                        285
                           65 SLAVSDLLVAVLVMPWKAVAEIAGFWPFGS-FCNIWVAFDIMCSTASILNLCVISVDRYW 123
                                                                                                                                                                                              240
SLAFADLLYSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                              121 AICCQPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
                                                                                                                                              124 AI-SSPFRYERKATPKAAFILISVAMTLSVLISFIPVQLSWHKAKPTSPSDGNVTSLGKT 182
                                                                                                                                                                                                                                                                                          241 QMLQRAGASSE-----SRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCW 286
                                                                                                                                                                                                                                                                                                                                                                                        287 APFFVTNIVDPFI-----DYTVPGOVWTAPLWLGYINSGINPFLYAFLNKSFRRAFLII 340
                                                                                                                                                                                                                                                                                                                      286 IPFFILNCMVPFCGSGETKPFCIDSITFDVFVWFGWANSSLNPIIYAF-NADFRKAFSTL
                                                                                                                                                                                              181 FHAIEKRKFNQNSNSTYCVFMVNXPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHOI
                                                                                                                                                                                                                        183 TH-------NCDSSLSRTYAISSSLISFYIPVAIMIVTYTRIYRIAQKOIRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-95024150; PubMed=7937989; Sugamori K.S., Demchyshyn L.L., Chung M., Niznik H.B.; Sugamori K.S., Demchyshyn L.L., Chung M., Niznik H.B.; Sugamori K.S., Demchyshyn L.L., Chung M., Niznik H.B.; Proc. or L. Acad. Sci. U.S.A. 91:10536-10540(1994).

1- FUNCTION: This is one of the five types (D1 to D5) of receptors for dopamine. The activity of this receptor is mediated by G for dopamine. The activity of this receptor is mediated by G proteins which activate ademylyl cyclase.

1- SUBCELLULAR LOCATION: Integral membrane protein.

1- TISSUE SPECIFICITY: Brain and kidney.

1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 LCCDDERYRRPSILGQTVPCSTTTI-----NGSTHVLRDAVECGGWESQCH 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGC----YR-----LCPTSTNAIRTVSINNWGAVVFSSHHEPRGSISKDCN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D(1C) dopamine receptor.
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PRO0237; GPCRRHODOPSN.
PROSITE; PRO0237; GPCRRHODOPSN.
PROSITE; PSO0227; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
DOMAIN 3 STRACELLULAR (POTENTIAL).
TRANSMEM 31 (TOTENTIAL).
TRANSMEM 55 65 CYTOPLASMIC (POTENTIAL).
TRANSMEM 59 2 (POTENTIAL).
DOMAIN 51 101 EXTRACELLULAR (POTENTIAL).
DOMAIN 53 101 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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PIR; IS1661; IS1661.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm.1; 1.
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01-NOV-1995 (Rel. 32, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIBKRKFNQNSNSTYCVFMVNKP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LNGVNHTENCDSSLNRT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 HRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFIDYTVPGO-------VWTAF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 -SFRKETXVLXTLSIIMGVFVFCWLPFFVLNCMIPFCHM\LPGQNEPEPPCVSETTFNIF 313
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                                                                                                                                                                                                                                                                                                                                                                                                               35 LSLLILSTLLGNTLVCLAVIKFRHLRSKVTNFFVISLAVSDLFVALLVMPWKAVTBVAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDINE=9236540; PubWed=1533268; MEDLINE=9236540; PubWed=1533268; Machida C.A., Searles R.P., Nipper V., Brown J.A., Kozell L.B., Nave K.A., "Molecular cloning and expression of the rhesus macaque D1 dopamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor gene.";
Mol. Pharmacol. 41:652-659 (1992).
Mol. Pharmacol. 41:652-659 (1992).

-!- FUNCTION: This is one of the five types (D1 to D5) of receptors for dopamine. The activity of this receptor is mediated by G proteins which activate ademylyl cyclase.
-!- SUBNIT: Interacts with calcyon (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                          6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
DRD1.
Macaca mulatta (Rhesus macaque).

Macaca mulatta (Rhesus macaque).

Macaca mulatta (Rhesus macaque).

Macaca mulatta (Rhesus macaque).

Macaca mulatta (Rhesus macaque).

Mamalia; Eutheria; Primates; Cararrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                    -palmitoyl cysteine (By similarity)
F41DF85AF0D2F869 CRC64;
                                                                                                                                                                                                                                                                                                                                                      36
                                                                                                                                                                                                                                                                                                                Length 465;
                                                                                                                                                                                                                                                                                                             ; Score 580; DB 1; Length 465; Pred. No. 1.7e-35; 53; Mismatchee 114; Indels
                                    4 (POTENTIAL). EXTRACELLULAR (POTENTIAL)
                  CYTOPLASMIC (POTENTIAL).
                                                                           5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
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124
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1168
1193
2219
2291
2394
465
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                                                                                                                                                                                                                                                                                                                                  Similarity
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CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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N-LINKED (GLUNAC. .) (POTENTIAL).

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N-LINKED (GLUNAC. .) (POTENTIAL).

N-LINKED (GLUNAC. .) (POTENTIAL). S-palmitoyl cysteine (By similarity) S-palmitoyl cysteine (By similarity) DFBGB9D765D600A5 CRC64; RRAFLIILCCDDERYRRPSILGQTVPCSTTTING----STHVLRDAV--EC 378 DB 1; Length 446; EMBL; AF077862; AAC27328.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Prints, PR00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1 2; 1.
PROMILY COUDIED RECEP_F1 2; 1.
PROMIN 24 49 1 (POTENTIAL). Query Match 27.2%; Score 579.5; DB 1; Length Best Local Similarity 33.7%; Pred. No. 1.7e-35; Matches 139; Conservative 67; Mismatches 135; Indels 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 49292 MW; 351 446 AA; 24 50 61 88 88 87 97 139 219 DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN LIPID DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN CARBOHYD CARBOHYD DISULFID 181 222 280 334 338 166

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                                                                                                                                                                                                                                                                                                                                                         APPROXIMATIVELY EQUAL AFFINITY.
SUBCELLULAR LOCATION: Integral membrane protein.
PTM: Homologous desensitization of the receptor is mediated by its phosphorylation by beta-adrenergic receptor kinase.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                            MEDILE 99129665; PubMed-78121;
Jung H., Windhaber R., Palm D., Schnackerz K.D.;
Jung H., Windhaber R., Palm D., Schnackerz K.D.;
Jung H., Windhaber R., Palm D., Schnackerz K.D.;
Introdular intracellular loop of the beta-adrenoceptor.";
FERS Lett. 358:133-136(1995).
-!- FUNCTION: BETA-ADRENREGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENTIATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
                                                                                                                                                                                         Ross E.M.; "The avian beta-adrenergic receptor: primary structure and membrane
                                                                                 Meleagris gallopavo (Common turkey).
Mukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris;
NCBL_TaxID=9103;
                                                                                                                                                                   Yarden Y., Rodriguez H., Wong S.K.-F., Brandt D.R., May D.C.,
Burnier J., Harkins R.N., Chen E.Y., Ramachandran J., Ullrich A.,
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PDB; 1DEP; 14-0CT-96.

InterPro; IPRO0275; GPCR.Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitat.
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Proc. Natl. Acad. Sci. U.S.A. 83:6795-6799(1986)
                                              01-APR-1988 (Rel. 07, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Beta-1 adrenergic receptor (Beta-T).
            483 AA
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Yarden Y., Rodriguez H., Wong S.K.
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            STANDARD;
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Leunissen J.A.M., Flik G., Wendelaar Bonga S.E., Martens G.J.M.;
Leunissen J.A.M., Flik G., Wendelaar Bonga S.E., Martens G.J.M.;
"Cloning and sequence analysis of a hypothalamic cDNA encoding a D1c
dopamine receptor in tilageia.";
Biochim. Biophys. Acta 1308:17-22(1996).
-!- FUNCTION: This is one of the five types (D1 to D5) of receptors
for dopamine. The activity of this receptor is mediated by G
proteins which activate adenylyl cyclase.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                       Gaps
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Labroidei,
Cichlidae, Oreochromis.
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Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
                                                                                                                                                                                       48;
                                                                                                         Length 483;
                                                                                                                                                                                       Indele
                               54078 MW; B11A7E71F6CCE3E4 CRC64;
                                                                                                                                                                                   57; Mismatches 135;
                                                                                                         26.9%; Score 574; DB 1; 37.0%; Pred. No. 4.7e-35;
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01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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earch completed: August 5, 2004, 13:34:49 ob time : 14 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. M protein - protein search, using sw model un on: August 5, 2004, 13:32:29; Search time 39 Seconds (without alignments) 3252.265 Million cell updates/sec	itle: erfect score: 2133 equence: 1 MDKLDANVSSEEGFGSVEKVESQCHPPATSPLVAAQPSDT 402 coring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	earched: 1017041 segs, 315518202 residues otal number of hits satisfying chosen parameters: 1017041	inimum DB seq length: 0 aximum DB seq length: 2000000000	Ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		#: bp_invari: 5: sp_invari: 6: sp_mammal:* 7: sp_mbc:* 8: sp_organelle:* 9: sp_phage:*	 14: sp_unclassified:* 15: sp_rvirus:* 16: sp_larisp:* 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q8ixh9 homo sapien 096ki0 homo sapien	Q29007 sus scrofa	OSmtw6 spisula sol	Ogvcz3 drosophila	042315 cyprinus ca	098842 anguilla an	Q8k4z4 cavia porce	Q98841 anguilla an	Q8wnd7 bos taurus	Q98844 anguilla an	Q98843 anguilla an	Q8neg8 homo sapien	096716 branchiosto	O9nhf3 aplysia cal
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26.0	26.0	25.9	25.9	25.9	25.9	25.9	25.8	25.7	25.7	25.7	25.7	25.7	25.6	25.6	25.6	25.6	25.5	25.3	25.2	25.1	25.0	25.0	24.7	24.6	24.5	24.4	24.4	
555 655	554.5	552.5	552.5	ĽΩ	552	552	550.5	548.5	548.5	548	548	547.5	547	546	546	545.5	543	539.5	537	535.5	534	532.5	526	524.5	523,5	520.5	520	2
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ALIGNMENTS

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TISSUE=Coronary artery;

XX MEDINE=95186798; PubMed=7656980;
XX Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
A Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
A Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
A Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
A Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;

RESP. 248176; Cakes1995.

RESEL 248176; Cakes1995.

RESEL 248176; Cakes1995.

RESEL 248176; Cakes1995.

RESEL 248176; Cakes1997.

RESEL 248176
                                                                                                                120
                                                                                                                                                  61 SLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYY 120
                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 QMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 CCQPLVYRNKWTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 YIVPGOVWTAFIWLGYINSGINPFLYAFLNKSFRRAFLIILCCDDERYRRFSILGGIVPC
121 AICCOPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD
                                                                                                                                                                                                                                                                                                     ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
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                                                                                                                                                                                                                                                                                                                                                                                                       181 FHAIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823,
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Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
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151 AA; 17240 MW; 6505B7CB46328750 CRC64;
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32.8%; Score 700; DB 6;
Best Local Similarity 85.4%; Pred. No. 2.5e-60;
Matches 129; Conservative 8; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                   AICCOPLVYRNXMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLBRSLNQGLGQD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 OMLORAGASSESRPOSADOHSTHRMRTETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID 300
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Yilaro M.T., Domenech T., Palacios J.M., Mengod G.;

Yariants including an ovel variant that lacks the alternatively spliced C-terminal exon.;

Usumitted (SEP-2000) to the EMEL/Genbank/DDBJ databases.

YILLARITY: BELOWGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

REMEL, AJ278979; CAC22248.1; -.. Membrane; IEA.

REMEL, AJ278979; CAC22248.1; -.. Membrane; IEA.

RO; GO:0001684; F:rhodopsin-like receptor activity; IEA.

RO; GO:0007186; P:-Protein coupled receptor protein signalin. .; IEA.

RO; GO:0007186; P:-Protein coupled receptor protein signalin. .; IEA.

RRINTS: PRO0227; GPCR_Rhodpsn.

RRINTS: PRO0217; GPCR_Rhodpsn.
                                                                                                             1 MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                AICCQPLVYRNKYTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 PHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                         0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 STTTINGSTHVLRDAVECGGOWESRCHPPATSPLVAAOPSDT 388
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
   96.3%; Pred. No. 1.3e-190; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-hydroxytryptamine4 receptor.
                                     387, Conservative
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   Best Local Similarity
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Best Local 8
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QBMTW6
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                                                                                                                        셤
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MEDLINE-99044151; PubMed=9826915;
MEDLINE-99044151; PubMed=9826915;
MEDLINE-99044151; PubMed=9826915;
Hirano J., Archer S.N., Djamgoz M.B.A.;

D2-like receptor a.

Requencing and comparison of five D1-like and three D2-like receptor R. SIMILARITY:
HELONGS TO FAMILY 1 OF G-PROTEIN (BY SIMILARITY).
HELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
REMBL; V14627; CAA74971.1;
CG: GO:0016021; C:integral to membrane; IEA.
GG: GO:0016021; C:integral to membrane; IEA.
RG: GO:00101601; Tal. 1.
RRINTS; PRO0237; GPCR.Rhodpsn.
RPGSITE; PSOS262; GPCR.Rhodpsn.
RPGSITE; PSOS262; GPCR.Rhodpsn.
RPGSITE; PSOS262; GPCREIN RECEP F1.; 1.
RPRINTS; PRO0237; GPROTEIN RECEP F1.; 1.
RPGSITE; PSOS262; GPROTEIN RECEP F1.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                       61 VIEKRKFHQNSNSTYCIFMVNKPYAITCSVVAFYIPFLLMVLAYWRIYYTAKEHAHQIQM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 PADLLVSVLVMPFGAIBLVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 COPLUYRNYMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 IEKRKFNQNSNSTY-----CVFMVNKPYALICSVVAFYIPFLLMVLAYYRLYVTAKEH 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 AHQIQMLQRAGASSESRPQ-----SADQHSTHRM--RTETKAAKTLCIIMGCFCLCWAP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LDSSVSQR----NSSKRVLFGCFLSLLILFTLLGNTLVCAAVTKFRHLRSKVINFFVISLA 65
                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLA 63
AIEKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSPRYERKMTPKVARIMISLAWILSILISFIPVQLNWH---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinus carpio (Common carp).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Cyprinus.
NCBI_TaxID=7962,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.1%; Score 599; DB 13; Length 4
35.7%; Pred. No. 6.2e-50;
tive 63; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                           O42316;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DIA4 dopamine receptor.
                                                                                                                                                                              121 LORAGAPAEGRPPSADOHSTHRMRTETKAAK 151
                                                                                                                                                                                                                                                                                                         Ź
                                                                                                                                                        LORAGASSESRPOSADOHSTHRMRTETKAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.1
Best Local Similarity 35.7
Matches 142, Conservative
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
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                                                                                                                                                     243
                                                                                                                                                                                                                                                               SSULT 4
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77 VSLAFADFLVSILVMPFNASIAISGKWMFGRTMCDVFNSNDVLFSTASILHLCCISMDRY 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || ||:||| |::|| |: :|:
|137 IAI-IHPFKYQSKWTHFRVYVMIAITWISSILISYIPIQSHWYT-----TSD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 TLKVMAERPDD------CLFIVNKAYAVVSSSISFWIPCTIMVFVXLKIYMEARRQEKQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KEHAHQIQMLQRAGASSESRPQSADQHSTHRMRTETKAAKTLCIIMGCFCLCWAPFF-- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 VSLAFADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 YAICCOPLVYRNKMTPLRIALMIGGCWVIPTPISFLPIMQGWNNIGIIDLERSLNQGLGQ 179
289 FFVTNIVDPFID-----YTVPGQVWTAFLWLGYINSGINPFLYAFLNKSFRRAFLII- 340
                                 279 FPVLNCMVPFCNPNEGSDFFCISSTTFDVPVWFGWANSSLNPIIYAF-NAGFRKAFSILL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LDANVSSEEGFGSVEKVVLLTFLSTVILM----AILGNLLVMVAVCWDRQLRKIKTNYFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative G-protein coupled receptor.
Spisula solidissima (Atlantic surf-clam).
Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dube F., Legault S.;
Dube F., Legault S.;
Dube F., Legault S.;
Dube F., Legault S.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AV055377; AAL23575.1;
EMBL; AV055377; AAL23575.1;
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:G-protein coupled receptor protein signalin.
Interpro; IPR00276; GPCR_Rhodpsn...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 AA; 44383 MW; C65E8AF910447347 CRC64;
                                                                                                                                                                   338 GCHRLCPGSNAIEIVSINNNGGPPSTSQYQPKGHVPKE 375
                                                                                                                               341 ----LCCDDERYRRPSILGQTVPCSTTTINGSTHVLRD 374
                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                           388 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm 1; 1. —
PRINTS; PR00237; GPCRADODSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                           PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mactroidea; Mactridae; Spisula.
NCBI TaxID=6584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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042315
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                                                                                                                                                                                                                                                                                                                    Addama M.D., Cellniker S.E., Holt R.A., Bvans C.A., Gocayne J.D.,
RA Addama M.D., Cellniker S.E., Holt R.A., W. Hoshins R.A., Galle R.F.,
George R.A., Lewis S.E., Holt R.A., W. Hoshins R.A., Galle R.F.,
RA damastides P.G., Scherer S.E. Li P.W. Hoshins R.A., Galle R.F.,
George R.A., Lewis S.E., Holt R.A., Sabburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pielifer B.D.,
RA Abril J.F., Adbayani A., An H. J., Andrews-Flemmkoh.C., Bardwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beseon K.Y. Benoes P.V. Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier R.,
RA Burtis K.C., Busam D.A., Butler H. Gddteu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahne C., Perrias C., Enrise P.,
RA de Rablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Cavler R.A., Cong F. C., Ferraz C., Ferraz C., Ferrias S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Guz S., Dunk V. B.C., Dunn P.,
Burtis K.C., Busam D.A. Home Z., Gang N.S., Celbart W.M., Glasser K.,
Alalali M., Kaluston K.A., Howland T.J., Hernandez J.R., Houck J.,
Alalali M., Kaluston K.A., Howland T.J., Hernandez J.R., Houck J.,
Alalali M., Kaluston K.A., Howlard T.J., Hernandez J.R., Houck J.,
Alalali M., Kaluston K.A., Howlard T.J., Hernandez J., Month E.I.,
Alasko P. Lei Y. Levitsky A.A., Liu J., Li Z., Liang Y., Lin X.,
R. Mattei B. McIncosh T.C., McLeod M.P., McPherson D.L.
RA Mount S.M., Nelson K.A., Moharry C., Morris J., Month S.M., Nelson D.L.
RA Menson D.R., Nelson K.A., Moharry C., Morris J., Month S.M., Wang X.,
Randon K., Reinger K., Saudders R.D.C., Scheeler F., Shen H.
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Rangoro M., Pittman G.S., Pan S., Pollard J., Puri, V. Ressen M.G.,
Rangoro M., Pittman G.S., Pan S., Pollard J., Puri, W. Wang Z.-Y.
Rangoro M., Rangoro M., Rubing M., Stupski M., Stape S., Zho S., Smith H.O.,
R. Melson D.Y., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; F:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR00276; GPCR_Rhodpsn.
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                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.1%; Score 598.5; DB 5; Length 508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0237; GPROTEIN PREEP F1 1; 1.
PROSITE; PS00237; G PROTEIN PREEP F1 1; 1.
PROSITE; PS50262; G PROTEIN PREEP F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 508 AA; 56855 MW; 02C7C335676EAEFO CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 8.2e-50;
                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0038980; CG6919.
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Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00001; 7tm
                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=7227;
                                                       CG6919 protein.
                                                                                                                                                                                                                                                          SEQUENCE
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12;
94 STDDADGSSHLALVFVKCFIIGFIILAAILGNMLVIVSVMRHRKLR-IITNYFVVSLAVA 152
                                                                                                                                                                                                                                                              -----YTTTE 252
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                                                                                                                                                                                                                                                                                                                                                              309 SKVAALLLEKHLQISQIPKPRPSIQVEQSTISTWRRERKAARTLGIIMSAFLICWLPFFL 368
                                                                                                                                                                                            126 PLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMOGWNNIGIIDLERSLNOGLGODFHAIB 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 AGASS-------ESRPQ-SADQHSTHRMRTETKAAKTI,CIIMGCFCLCWAPFFV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 PADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y14626; CAA74970.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001682; F:receptor activity; IEA.

GO; GO:0001584; F:receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

InterPro; IPR00276; GPCR_Rhodpsn.
                                                                                            186 KRKFNONSNSTYCVFMVNKFYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQIQMLQR
                                                             DLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIPHLCCISLDRYYAICCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Retina;
MEDLINE=99044151; PubMed=9826915;
Hirano J., Archer S.N., Djamgoz M.B.A.;
"Dopamine receptor subtypes expressed in vertebrate (carp and eel)
retinae: cloning, sequencing and comparison of five D1-like and three D2-like receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 LDSSVSQR----NSSKRVITGCFLSLLIMTTLLGNTLVCAAVTKFRHLRSKVTNFFVISLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LDANVSSEEGFGSVEKVVLLIFLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recept. Channels 5:387-404(1998).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 TNIVDPFIDYTVPGQVWTAFL-WLGYINSGLNPFLYAFLNKSFRRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 PLDYPLIMTQRRVFIMLLMVWLSPALLSFLPICSGW------
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PROSITE; PS00237; GPCRAHODOPSN.
PROSITE; PS00262; G-PROTEIN RECEP_II; 1.
PR05ITE; PS50262; G-PROTEIN RECEP_III; 1.
SEQUENCE COUPLEd receptor; Receptor; Transmembrane.
SEQUENCE 446 AA; 49800 MW; 417034A303627D20 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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124 CQPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHA 183

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9 SSEEGFGSVEKVVLLT---FLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLAFA

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66 VSDLLVAILVMPWKAVTEVAGFWPFGS-FCNIWVAFDIMCSTASILNLCIISVDRYWAI- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 22, TremBLrel. 22, TremBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta2-adrenergic receptor.
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J. Biol. Chem. 272:2778-278-7807(1997).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SUBCELLULAR TY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL; UG2919; AAC60069-1; -- membrane; IEA.

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:000184; F:receptor activity; IEA.

GO; GO:000184; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:subtilase activity; IEA.

GO; GO:000186; P:subtilase activity; IEA.

GO; GO:0002080; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000209; GPGR Rhodpsn.

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                                                                             184 IEKRKFNQNSNSTY-----CVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEH 236
                                                                                                             -----HK 163
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                                                                                                                                                                                237 AHOLOMLORAGASSESRPO----SADOHSTHRM--RIETKAAKTLCIIMGCFCLCWAP
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Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.B.,
                                                                                                                                                                                                                                                                                                                                                                                      341 ----LCCDDERYRRPSILGQTVPCSTTTI-----NGSTHVLRDAVEC 378
                                                                                                                                                                                                                                                                                                                                                                                                                    52;
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PRINTS, PRO0237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECR. F1 1; 1.

PROSITE; PS00136; GPROTEIN RECR. F1 2; 1.

PROSITE; PS00136; SUBTILASE ASP; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 445 AA; 49310 MM; B443ADABICICI439 CRC64;
SPFRYERKWTPKVAFIMISVAWTLSILISFIPVQLNW----
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Last sequence update)
Last annotation update)
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MEDLINE=97160583; PubMed=9006917;
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Best Local Similarity
Matches 132; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7936;
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                                                                                                                                                                                                                                     184 IEKRKFNONSNSTY-----CVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEH 236
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124 CQPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordafa, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Cavidae, Cavia.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS02337; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
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Matches 135, Conservative
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12. J. Biol. Chem. 272:2778-2787(1997).
13. Biol. Chem. 272:2778-278-278-2787(1997).
14. J. SIMCLALIULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
15. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
16. Refl., U62918; AAGG0067.1; -
17. Chem. 27. Chem. 
                                                                                                                                                                                                                                                                                            295 VHVIQDNLIPKEVYILLAWVGYVNSAFNPLIYC-RSPDFRIAFQELLC----LRRSALK 348
EXEKFNONSNSTYCVFMVNKPYALTCSVVAFYLPFILMVLAYYRIYVTAKEHAHQIQMLQ 244
                                 295 VDPFIDYTVPGQVWTAFLWLGYINSGLNPFLYAPLNKSFRRAFLIILCCDDERYRRPSIL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 FADLLVSVLVMPFGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAIC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CQPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNN---IGIIDLERSLNQGLGQD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHAIBKRKFNQNSNSTYCVFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAHQI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vertebrates. Molecular phylogenetic, pharmacological, and functional
criteria defining DIA, DIB, and DIC receptors in European eel Anguilla
anguilla.";
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                                                                                                                                                                                                                                                                                                                                                                                                                      349 AYGNDCSSNS NGKTDYTGEPNVCHQGQEKERELLCEDPPGTEDLVSCPGTVPSDS 403
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                                                                                                                                                                                                                                                                                                                                                                                 355 GQTVPCSTTTINGSTHVLRDAVEC -- GGGWESQ -- CH-PPATSPLVAAQ --- PSDT 402
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Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AICCQPLVYRNKMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQD 180
                                                                             241 OMLORAGASSESR----POSADQHSTHRM--RTETKAAKTLCIIMGCFCLCWAPFFVTNI 294
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                                                                                                                                                                                295 VDFFIDYT------VPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRAFLILCC 343
                                                                                                                                                                                                         288 MVPFCEQAPQGAADLPCVSSTTFDVFVWFGWANSSLNPIIYAF-NADFRKAFSTLLGC 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AI-SSPFRYERKMTPKAAFILISVAWTLSVLISFIPVQLSWHKAKPTGPSEGNATSLGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FHAIEKRKFNONSNSTYCVFMVNKPYAITCSVVAPYIPFLLMVLAYYRIYVTAKEHAHQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 QMLQRAGASSE-----SRPQSADQHSTHRMRTETXAAKTLCIIMGCFCLCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping.";
substitution to the EMBL/GenBank/DDBJ databases.
substitution LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Haegeman A., Peelman L.; Haegeman A.A., Jacobs K., van Zeveren A., Peelman L.; "Bovine dopamine lA receptor: cDNA sequence, polymorphisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PROOZ37; GPCTRHODOPSN.
PROSTTE; PS00237; GPOTEIN RECEP F1 1; 1.
PROSTTE; PS50262; G-PROTEIN RECEP F1 2; 1.
G-procein coupled receptor; Receptor; Transmembrane.
SEQUENCE 446 AA, 49316 MW; 00F13996BA7CBBEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                    RESULT 13
Q98843
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1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
2. 1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
3. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
4. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
5. MEL; U62921; AACGO068.1; --
6. GO; 000.0004872; F:receptor activity; IEA.
6. GO; 000.0186; P:receptor activity; IEA.
6. GO; 000.0186; P:rendopsin-like receptor protein signalin. .; IEA.
7. Interpro; IRPRO0276; GPCR_Rhodpsn.
7. R PROSITE; PRO0237; GPROTEIN RECEP F1 1; 1.
7. PRINTS; PRO0237; GPROTEIN RECEP F1 2; 1.
7. PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
7. G-protein coupled receptor; Receptor; Transmembrane.
7. SEQUENCE 448 AA; 50084 MM; OABCO296650B29F3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 WIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAICCQPLVYRNKWFPLRIALMLGGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIEKRKFNQNSNSTYCVFWVNXP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 WILSILISFIPVQLNWHK------ABEDYADD----NSSNHTEDCNASINST 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAITCSVVAFYIPFLLMVLAYYRIYVTAXEHAHQIQMLQRAGASSESRPQSADQHSTHRM 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT----ETKAAKTLCIIMGCFCLCWAPFFVTNIVDPFID-----YTVPGQVWTAFLWL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 LPFFILNCMVPFCGSGETKPFCIDSITFDVFVWFGWANSSLNPIIYAF-NADFRKAFSTL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 LSTVILMAILGNILVMVAVCWDRQLRKIKTNYFIVSLAFADLLVSVLVMPFGAIELVQDI 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vertebrates. Molecular phylogenetic, pharmacological, and functional criteria defining DIA, DIB; and DIC receptors in European eel Anguilla
                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
Anguilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=97160583; PubMed=9006917;
Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.7%; Score 569; DB 13; Length 448; 37.9%; Pred. No. 5.5e-47; tive 59; Mismatches 114; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Early emergence of three dopamine D1 receptor subtypes in
                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                    LCCDDERYRRPSILGQTVPCSTTTINGSTHVL 372
                                                                       345 LGC----YRLCPTTNNAI--ETVSINNNGAVV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYINSGLNPFLYAFLNKSFRRAFLIILCCD 344
                                                                                                                                                                                                                                                                                                 Anguilla anguilla (European freshwater eel)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 37.9
Matches 125, Conservative
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel. 01-FEB-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                              Dopamine DlC receptor.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7936;
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                                    341
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PERYERRATORVAFVAISVTWTLSVLISFIPVQLAWHKAS--DEEVWIN---GISF---- 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GEKSENCDSSLNREYAISSSLISPYIPVAIMIVTYTRIYRIAQIQIRRISSLER 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 PLVYRNKOMTPLRIALMLGGCWVIPTFISFLPIMQGWNNIGIIDLERSLNQGLGQDFHAIE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 AGASSES---RPQSADOHSTHR--MRTETKAAKTLCIIMGCFCLCWAPFFVTWIVDPFID 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y------TVPGQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRR 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 RPPTDHTAGLPCVSDTTFDVFVWFGWTNSSLNPIIYAF-NADFRKAFASLLGCRNFCSRT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DILVSVLVMPRGAIELVQDIWIYGEVFCLVRTSLDVLLTTASIFHLCCISLDRYYAICCQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vertebrates. Molecular phylogenetic, pharmacological, and functional criteria defining DlA, DlB, and DlC receptors in European eel Anguilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEEGFGSVEKVVLLT---FLSTVILMAILGNLLVMVAVCWDRQLRKIKTNYFIVSLAFA
                                                                                                                                                                                                                                                                                                Anguilla anguilla (European freshwater eel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.4%; Score 564; DB 13; Length 458; Best Local Similarity 35.4%; Pred. No. 1.7e-46; Matches 141; Conservative 63; Mismatches 148; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Early emergence of three dopamine D1 receptor subtypes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P--..SILGQTVPCSTTT----INGSTHVLRDAVEC 378
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                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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312 GWANSSINPVIYAF-NADFRKAFSTILGCN 340
                                                                                                                           458
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97160583; PubMed=9006917;
                                                                                                                                                                     (TrEMBLrel. 02, C
(TrEMBLrel. 02, L
(TrEMBLrel. 24, L
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                 Dopamine D1B receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 IELVQDIWIYGEVFCLVRISLDVLLTTASIFHLCCISLDRYYAICCOPLVYRNXWTPLRI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 ALMLGGCWVIPTFISFLPIMQGWN----NIGIIDLERSLNQGLGQDFHAIEKRKFNQNS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 PQSA----DQHSTHRMRTETKAAKTLCIIMGCFCLCWAPPFVTNIVDPFIDYTVPG---- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 RSSAACAPDXSLRASIKKETKVLKTLSVIMGVFVCCMLPFFILNCMVPFCSGHPEGPPAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 KVVLLFFLSTVILMAILGNLLVMVAVCMDRQLRKIKTNYFIVSLAFADLLVSVLVMPFGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

A Publ H.L. III, Ikeda S.R., Aronstam R.S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL, AVI36750; AAN01276.1; -..

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; OO:001584; F:rhodopsin-like receptor activity; IEA.

R GO; GO:0001186; P:rhodopsin-like receptor protein signalin. . .;

R InterPro; IPR000276; GPCR.Rhodpsn.

R PRINTS; PR00237; GPRRHODOPSN.

R PRINTS; PR00237; GPRRHODOPSN.

R PROSITE; PS00237; GPROTEIN_RECEP_FI_2; 1.
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.4%; Score 563.5; DB 4; Length Best Local Similarity 34.7%; Pred. No. 2e-46; Matches 137; Conservative 69; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 AA; 52960 MW; FFB0B7662D368AF2 CRC64;
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Last annotation update)
                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 AA
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                                                                                                                         Created)
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                                                                                                                                               (TrEMBLrel. 22, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 10, (TrEMBLrel. 10, (TremBlrel. 24,
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                                                           PRELIMINARY;
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                                                                                                                   (TrEMBLrel.
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-: SUBCELDUAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-: SUBCELDUAR TO SAUGEST OF FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJO05433; CAA06536.1;
EMBL; AJO05631; Cintegral to membrane; IEA.
GO; GO:00016031; F:receptor activity; IEA.
GO; GO:0001684; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
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                                                                                                                                Cardinaud B., Gibert JM., Sugamori K.S., Coudouel S., Guibert B., Vincent J.D., Niznik H.B., Vernier P.; "The amphioxus DI/beta receptor and the emergence of the vertebrate
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Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
Bukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae;
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PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

GPOSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-PTOLEIC; DS00262; G PROTEIN RECEP F1 2; 1.

GPOSITE; PS30162; GROUPEN RECEP F1 2; 1.

GROUPING Z PROTEIN RECEP F1 2; 1.

GROUPING Z PROTEIN RECEP F1 2; 1.
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38.5%; Pred. No. 2.3e-46;
cive 57; Mismatches 117,
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Matches 135, Conservative
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